

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:36:05 ; Search time 24.74 Seconds
(without alignments)

400.655 Million cell updates/sec

Title: US-09-824-134-2

Perfect score: 1302

Sequence: 1 VNOAPECRFGGILPLGKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	79.9	208	1	FADD_HUMAN
2	719.5	55.3	205	1	FADD_MOUSE
3	122	9.4	479	1	ICSE_HUMAN
4	121.5	9.3	1880	1	ANK1_HUMAN
5	117.5	9.0	1862	1	ANK1_MOUSE
6	115.5	8.9	656	1	RIP_MOUSE
7	111.5	8.6	671	1	RIP_HUMAN
8	110	8.4	480	1	CFLA_HUMAN
9	108	8.3	521	1	ICSE_HUMAN
10	99	7.6	324	1	ANK2_HUMAN
11	98.5	7.6	444	1	DYHC_MOUSE
12	98.5	7.6	484	1	DYHC_RAT
13	96.5	7.4	535	1	HTR1_HALSA
14	95.5	7.3	497	1	RP54_PSEAE
15	93.5	7.2	324	1	TNR6_RAT
16	91.5	7.0	470	1	ARYL_MYCTU
17	91.5	7.0	1816	1	LMA4_HUMAN
18	91	7.0	3695	1	LMA5_HUMAN
19	90.5	7.0	130	1	PE15_MOUSE
20	90.5	7.0	411	1	KICL_RABIT
21	90	6.9	295	1	X769_HUMAN
22	90	6.9	953	1	Y442_HUMAN
23	89.5	6.9	535	1	HPFL_HALNI
24	89.5	6.9	962	1	ARVC_HUMAN
25	89	6.8	483	1	KICL_MOUSE
26	88.5	6.8	130	1	PE15_HUMAN
27	88.5	6.8	892	1	AAAC1_HUMAN
28	88.5	6.8	893	1	AAAC1_CHICK
29	87.5	6.7	433	1	CGBL_HUMAN
30	87.5	6.7	484	1	CFLA_MOUSE
31	87.5	6.7	894	1	CFLA_MOUSE
32	87.5	6.7	3433	1	UTRO_HUMAN
33	87	6.7	332	1	TNR6_PIG
					Q13158 homo sapien
					Q61160 mus musculu
					Q14790 h caspase-8
					P16157 homo sapien
					Q02357 mus musculu
					Q60855 mus musculu
					Q13546 homo sapien
					Q15519 h casp8 and
					Q02851 homo sapien
					Q01484 homo sapien
					Q97hu4 mus musculu
					P38650 rattus norv
					P33955 halobacteri
					P49988 pseudomonas
					Q63199 rattus norv
					P49994 mycobacteri
					Q16363 homo sapien
					Q15230 homo sapien
					Q62048 mus musculu
					Q28706 oryctolagus
					Q99871 homo sapien
					Q9upv9 homo sapien
					P33741 halobacteri
					Q00192 homo sapien
					Q64291 mus musculu
					Q15121 homo sapien
					P12814 homo sapien
					P05094 gallus gall
					P14635 homo sapien
					Q35732 m casp8 and
					Q9j191 mus musculu
					P46939 homo sapien
					Q77736 sus scrofa

34 86.5 6.6 294 1 PARB_CAUCR
35 86.5 6.6 1073 1 MTR4_YEAST
36 86 6.6 587 1 YCAQ_HAEIN
37 86 6.6 1453 1 Y373_BOVIN
38 85.5 6.6 880 1 RASO_PYRAB
39 85 6.5 899 1 PLCL_SCHPO
40 84.5 6.5 892 1 AACL_RAT
41 84.5 6.5 903 1 YB56_METJA
42 84 6.5 209 1 TRIC_HUMAN
43 84 6.5 1957 1 YD86_SCHPO
44 83.5 6.4 171 1 CFLA_HSV2
45 83.5 6.4 283 1 LECH_MOUSE

ALIGNMENTS

RESULT 1
FADD_HUMAN STANDARD; PRT; 208 AA.
AC Q13158; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (FAS-associating death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MORTL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC TISSUE-Umbilical vein endothelial cells;
RX MEDLINE=95277837; PubMed=7538907;
RA Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT "FADD, a novel death domain-containing protein, interacts with the
RT death domain of Fas and initiates apoptosis.";
RL Cell 81:505-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95229578; PubMed=7536190;
RA Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA Wallach D.;
RT "A novel protein that interacts with the death domain of Fas/AP01
RT contains a sequence motif related to the death domain.";
RL J. Biol. Chem. 270:7795-7798(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RN [4]
RP Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RT STRUCTURE BY NMR OF 1-83.
RX MEDLINE=98241233; PubMed=9582077;
RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA Lenardo M.J., Fesik S.W.;
RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT domain";
RL Nature 392:941-945(1998).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS.
CC -1- SUBUNIT: INTERACTS WITH CFLAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT
CC FOR PERIPHERAL BLOOD MONONUCLEAR LEUKOCYTES.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

O05190 caulobacter
P47047 saccharomyc
P44144 haemophilus
Q9tu23 bos taurus
Q9uzc8 pyrococcus
Q90977 schizosacch
Q921p2 rattus norv
Q58556 methanococc
P19429 homo sapien
Q10411 schizosacch
Q66674 equine herp
P34927 mus musculu

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 CC -----
 DR EMBL; U24231; AAA86517.1;
 DR EMBL; X84709; CAA59197.1;
 DR EMBL; BC000334; AAH00334.1;
 DR PDB; 1A1W; 16-FEB-99.
 DR PDB; 1A1Z; 16-FEB-99.
 DR MIM; 602457;
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 DR Apoptosis; 3D-structure.
 DR DOMAIN 3 81
 DR MUTAGEN 97 181
 DR FT MUTAGEN 121 121
 DR FT CONFLICT 32 32
 DR FT CONFLICT 32 32
 DR SQ SEQUENCE 208 AA; 23279 MW; 065E2F852E83507 CRC64;

Query Match 79.9%; Score 1040; DB 1; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.2e-74;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

Query Match 79.9%; Score 1040; DB 1; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.2e-74;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 2
 FADD_MOUSE
 ID FADD_MOUSE
 AC Q61160; 061082; STANDARD; PRT; 205 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FADD protein (FAS-associated death domain-containing protein)
 GN (Mediator of receptor induced toxicity).
 GN FADD OR MORT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96220459; PubMed-8649383;
 RA Zhang J., Winoto A.;
 RT "A mouse Fas-associated protein with homology to the human MORT1/FADD
 RL protein is essential for Fas-induced apoptosis.",
 Mol. Cell. Biol. 16:2756-2763(1996).

RP SEQUENCE FROM N.A.
 RX MEDLINE-96152659; PubMed-8565075;
 RA Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
 RT "RAD3-TRAF2 and TRADD-FADD interactions define two distinct TNF
 RT receptor 1 signal transduction pathways.",
 RL Cell 84:299-308(1996).
 CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
 CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
 CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
 CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
 CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
 CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
 CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
 CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U50406; AAB07789.1;
 DR EMBL; U43184; AAA97876.1;
 DR HSP; Q13158; IALZ.
 DR MGD; MGI-109324; Fadd.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 DR Apoptosis.
 DR DOMAIN 3 81
 DR MUTAGEN 97 181
 DR FT CONFLICT 168 168
 DR FT CONFLICT 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;
 DR SQ SEQUENCE 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;
 QY 49 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 MDPLVLLHSVSSSSSELTELKFLGVRVKKRLRVQSGDLDFSMLEQNDLEPGHT 108
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 DB 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCFAAFNVICDNGKDWRLAROLK 168
 QY 169 VSDTKIDSDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 DB 121 VSEAKMDIEEKYPRSLSERVRESLRWKTEKENATVAHLVGLRSCQMNVLADLVQEV 228
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 DB 181 QES---VSKSENMPVLRDSTVSSE 203

RESULT 3
 ICEB_HUMAN
 ID ICEB_HUMAN
 AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;
 AC Q15806; Q9UQ81; Q14676;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FADD protein (FAS-associated death domain-containing protein)
 GN (Mediator of receptor induced toxicity).
 GN FADD OR MORT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96220459; PubMed-8649383;
 RA Zhang J., Winoto A.;
 RT "A mouse Fas-associated protein with homology to the human MORT1/FADD
 RL protein is essential for Fas-induced apoptosis.",
 Mol. Cell. Biol. 16:2756-2763(1996).

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OM nucleic - nucleic search, using sw model

Run On: August 17, 2002, 00:37:50 ; Search time 2174.44 Seconds
(without alignments)
16370.210 Million cell updates/sec

Title: US-09-824-134-1

Perfect score:

Sequence:

1 GTGAATCAGGACCGAGTG.....ACAAAAA.....1701

Scoring table:

IDENTITY_NUC

Gap 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description

RESULT	1	1701	100.0	1701	9	HSMRINTX
LOCUS	HSMRINTX	1672.8	98.3	1734	9	BC000334
DEFINITION	H. sapiens mRNA for mediator of receptor-induced toxicity.	1621.8	95.3	1642	9	HSU24231
ACCESSION	X84709	1326.4	78.0	1642	9	HSU74301
VERSION	X84709.1	1247.4	73.3	169725	9	AP000879
KEYWORDS	MORT1 gene.	728	43.4	143409	2	AP001787
SOURCE	human	429	27.0	78291	2	AC023216
ORGANISM	Homo sapiens	457	25.1	1634	2	HSU62022
REFERENCE		365.6	21.5	1497	10	BC004584
AUTHORS		365.6	21.5	1512	10	BC021400
TITLE		363.8	21.4	1377	10	MMU50406
JOURNAL		359	21.1	618	10	MMU43184
MEDLINE		341	20.0	143409	2	AP001787
REFERENCE		312.6	18.4	66127	2	AC067995
AUTHORS		288.8	17.0	298	6	AX138456
TITLE		62.2	3.7	39524	1	SCN10
JOURNAL		62	3.6	125020	9	AF429315
MEDLINE		60	3.5	200050	1	AL646068
REFERENCE		59.2	3.4	216050	1	SCE34
AUTHORS		58.6	3.4	2497	1	RSHEMZFN
TITLE		57.8	3.4	53184	2	AC110059
JOURNAL		57.2	3.4	158174	8	AP003414
MEDLINE		56.8	3.3	10948	1	AE005746
REFERENCE		56.8	3.3	171977	2	AC080022
AUTHORS		56.6	3.3	11886	1	AE004638
TITLE		56.4	3.3	125020	9	AF429315
JOURNAL		56.2	3.3	143278	2	OSJN00087
MEDLINE		55.6	3.3	24808	2	AC104312
REFERENCE		55.6	3.3	33820	1	SCE20
AUTHORS		54.8	3.2	18270	1	AF148496
TITLE		54.6	3.2	151773	8	AP001551
JOURNAL		54.4	3.2	150594	8	AP001859
MEDLINE		54.2	3.2	207683	2	AC098712
REFERENCE		53.8	3.2	4573	1	AB056583
AUTHORS		53.6	3.2	12249	1	AE004632
TITLE		53.6	3.2	108705	2	AP004182
JOURNAL		53.6	3.2	115154	2	AP003804
MEDLINE		52.8	3.2	272545	2	AC090533
REFERENCE		52.6	3.1	11059	14	PRVULGNS
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ALIGNMENTS

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

1701 bp mRNA linear PRI 27-APR-1995
H. sapiens mRNA for mediator of receptor-induced toxicity.

X84709.1 GI:791037

MORT1 gene.

human

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1701)

Boldin, M.P., Varfolomeev, E.E., Pancer, Z., Mett, I.L., Camonis, J.H.

and Wallach, D.

A novel protein that interacts with the death domain of Fas/AP01

contains a sequence motif related to the death domain

J. Biol. Chem. 270 (14), 7795-7798 (1995)

9529578

2 (bases 1 to 1701)

Wallach, D.

Direct Submission

Submitted (10-FEB-1995) D. Wallach, The Weizmann Institute, Dept of

Membrane Research & Biophysics, Rehovot 76100, ISRAEL


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SOURCE     Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1642)
AUTHORS   Kim,P.K.M., Dutra,A., Chandrasekharappa,S.C. and Puck,J.M.
TITLE     Genomic structure and mapping of human FADD, an intracellular
mediator of lymphocyte apoptosis
JOURNAL   J. Immunol. (1996) In press
REFERENCE 2 (bases 1 to 1642)
AUTHORS   Kim,P.K. and Puck,J.M.
TITLE     Direct Submission
JOURNAL   Submitted (13-OCT-1996) LCT, NCHCR, NIH, RM 3B07 Bldg. 49, 49

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: August 17, 2002, 00:37:50 ; Search time 2174.44 Seconds
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Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
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TITLE						
JOURNAL						

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DEFINITION	H.sapiens mRNA for mediator of receptor-induced toxicity.				
ACCESSION	X84709				
VERSION	X84709.1				
KEYWORDS	MOF1 gene.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
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JOURNAL	Boldin, M.P., Varfolomeev, E.E., Pancer, Z., Mett, I.L., Camonis, J.H.				
MEDLINE	and Wallach, D.				
REFERENCE	A novel protein that interacts with the death domain of Fas/APO1				
AUTHORS	contains a sequence motif related to the death domain				
TITLE	J. Biol. Chem. 270 (14), 7795-7798 (1995)				
JOURNAL	95239578				
	2 (bases 1 to 1701)				
	Wallach, D.				
	Submitted (10-FEB-1995) D. Wallach, The Weizmann Institute, Dept of				
	Membrane Research & Biophysics, Rehovot 76100, ISRAEL				

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U74301 Human FADD
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1642)
AUTHORS Kim, P. K. M., Dutra, A., Chandrasekharappa, S. C. and Puck, J. M.
TITLE Genomic structure and mapping of human FADD, an intracellular
mediator of lymphocyte apoptosis
JOURNAL J. Immunol. (1996) in press
REFERENCE 2 (bases 1 to 1642)
AUTHORS Kim, P. K. and Puck, J. M.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1996) LBT, NCHGR, NIH, RM 3807 Bldg. 49, 49

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Convent Dr., Bethesda, MD 20892-4442, USA
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QY 439 GCAGCATTTAACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 498
Db 424 GCAGCATTTAACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 499 CTCAGAGTCTCAGACACCAAGATCGACAGATCGAGGACAGATACCCCGCCACCTGACA 558
Db 484 CTCAGAGTCTCAGACACCAAGATCGACAGATCGAGGACAGATACCCCGCCACCTGACA 543
QY 559 GAGCGTGTGGGAGTCACTGAGAACTCTGGAAGAACACAGAGAGGAGAGCAACAGTG 618
Db 544 GAGCGTGTGGGAGTCACTGAGAACTCTGGAAGAACACAGAGAGGAGAGCAACAGTG 603
QY 619 GCCACCTGTGGGGCTCTCAGGCTCTGCCAGATGAACCTGTGGGTGACCTGGGTACAA 678
Db 604 GCCACCTGTGGGGCTCTCAGGCTCTGCCAGATGAACCTGTGGGTGACCTGGGTACAA 663
QY 679 GAGGTTCCAGAGCGCGCTGACCTCCAGACAGAGTGGGGCCATGTCCCGAGTGTATGG 738
Db 664 GAGGTTCCAGAGCGCGCTGACCTCCAGACAGAGTGGGGCCATGTCCCGAGTGTATGG 723
QY 739 AACTCAGACGATCTACCTCCGAGGCTCTGATGGCGGCTGCTTTGGCGCTGGTGGACC 798
Db 724 AACTCAGACGATCTACCTCCGAGGCTCTGATGGCGGCTGCTTTGGCGCTGGTGGACC 783
QY 799 ACAGGATCTACACAGCCTGGACTTTGGTTCTCTCAGGAGAGGTAGCCAGCACTGTGAA 858
Db 784 ACAGGATCTACACAGCCTGGACTTTGGTTCTCTCAGGAGAGGTAGCCAGCACTGTGAA 843
QY 859 GACCCAGCAGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGACTCAAGCTGC 918
Db 844 GACCCAGCAGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGACTCAAGCTGC 903
QY 919 GTTTATTAAATGCTCTCCCGCAGCAGCGGGCTTGGCGGCTGCACAGATATTTCCATTT 978
Db 904 GTTTATTAAATGCTCTCCCGCAGCAGCGGGCTTGGCGGCTGCACAGATATTTCCATTT 963
QY 979 CTTCTCTCATATGACACTGAGCAAGATCTTTGTTCTCCCACTAAATGAGCTCTCGGGAGTA 1038
Db 964 CTTCTCTCATATGACACTGAGCAAGATCTTTGTTCTCCCACTAAATGAGCTCTCGGGAGTA 1023

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: August 17, 2002, 00:36:05 ; Search time 24.74 Seconds

(without alignments)
400.655 Million cell updates/sec

Title: US-09-824-134-2

Perfect score: 1302

Sequence: 1 VNOAPECRFGGILGLPKRR.....RSGAMSPMWSNDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	79.9	208	1 FADD_HUMAN	Q13158 homo sapien
2	719.5	55.3	205	1 FADD_MOUSE	Q61160 mus musculus
3	122	9.4	479	1 ICE8_HUMAN	Q14790 h caspase-8
4	121.5	9.3	1880	1 ANK1_HUMAN	P16157 homo sapien
5	117.5	9.0	1862	1 ANK1_MOUSE	Q02357 mus musculus
6	115.5	8.9	656	1 RIP_MOUSE	Q60855 mus musculus
7	111.5	8.6	671	1 RIP_HUMAN	Q13546 homo sapien
8	110	8.4	480	1 CFLA_HUMAN	Q15519 h casp8 and
9	108	8.3	521	1 ICEA_HUMAN	Q92851 homo sapien
10	99	7.6	3924	1 ANK2_HUMAN	Q01484 homo sapien
11	98.5	7.6	4644	1 DYHC_MOUSE	Q9JHU4 mus musculus
12	98.5	7.6	4644	1 DYHC_RAT	P38650 rattus norv
13	96.5	7.4	535	1 HTR1_HALSA	P33955 halobacteri
14	95.5	7.3	497	1 RP54_PSEAE	P49988 pseudomonas
15	93.5	7.2	324	1 TNR6_RAT	Q63199 rattus norv
16	91.5	7.0	470	1 ARLY_MYCTU	P94994 mycobacteri
17	91.5	7.0	1816	1 LMA4_HUMAN	Q16363 homo sapien
18	91	7.0	3695	1 LMA5_HUMAN	Q15230 homo sapien
19	90.5	7.0	130	1 PE15_MOUSE	Q62048 mus musculus
20	90.5	7.0	411	1 K1CL_RABIT	Q28706 oryctolagus
21	90	6.9	295	1 X769_HUMAN	Q99871 homo sapien
22	90	6.9	953	1 YA42_HUMAN	Q99871 homo sapien
23	89.5	6.9	535	1 HTR1_HALN1	P33741 halobacteri
24	89.5	6.9	962	1 ARVC_HUMAN	Q00192 homo sapien
25	89	6.8	483	1 K1CL_MOUSE	Q64291 mus musculus
26	88.5	6.8	130	1 PE15_HUMAN	Q15121 homo sapien
27	88.5	6.8	832	1 AAC1_HUMAN	P12814 homo sapien
28	88.5	6.8	893	1 AAC1_CHICK	P05094 gallus gall
29	87.5	6.7	433	1 CGB1_HUMAN	P14635 homo sapien
30	87.5	6.7	484	1 CFLA_MOUSE	Q35732 m casp8 and
31	87.5	6.7	894	1 AAC2_MOUSE	Q9J191 mus musculus
32	87.5	6.7	3433	1 UTRC_HUMAN	P46939 homo sapien
33	87	6.7	332	1 TNR6_PIG	O77736 sus scrofa

34 86.5 6.6 294 1 PARB_CAUCR
35 86.5 6.6 1073 1 MTR4_YEAST
36 86 6.6 587 1 YCAO_HAEIN
37 86 6.6 1453 1 Y373_BOVIN
38 85.5 6.6 880 1 RA50_PYRAB
39 85 6.5 899 1 PLG1_SCHPO
40 84.5 6.5 892 1 AAC1_RAT
41 84.5 6.5 903 1 YB56_METJA
42 84 6.5 209 1 TRIC_HUMAN
43 84 6.5 1957 1 YD86_SCHPO
44 83.5 6.4 171 1 CFLA_HSV2
45 83.5 6.4 283 1 LECH_MOUSE

O05190 caulobacter
P47047 saccharomyc
P44144 haemophilus
Q9TU23 bos taurus
Q9U2C8 pyrococcus
P40977 schizosacch
Q9Z1P2 rattus norv
O58556 methanococc
P19429 homo sapien
Q10411 schizosacch
Q66674 equine herp
P34927 mus musculu

ALIGNMENTS

RESULT 1
FADD_HUMAN
ID FADD_HUMAN STANDARD; PRT; 208 AA.
AC Q13158; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FADD protein (FAS-associating death domain-containing protein)
DE (Mediator of receptor induced toxicity).
GN FADD OR MOR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS
RC TISSUE-Unbiblical vein endothelial cells;
RX MEDLINE=95277837; PubMed=7538907;
RA Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT "FADD, a novel death domain-containing protein, interacts with the
RT death domain of Fas and initiates apoptosis.";
RL Cell 81:505-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95229578; PubMed=7536190;
RA Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA Wallach D.;
RT "A novel protein that interacts with the death domain of Fas/AP01
RT contains a sequence motif related to the death domain.";
RL J. Biol. Chem. 270:7795-7798(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Lung;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP STRUCTURE BY NMR OF 1-83.
RX MEDLINE=98241233; PubMed=9582077;
RA Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA Lenardo M.J., Fesik S.W.;
RT "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT domain.";
RL Nature 392:941-945(1998).
CC -1- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS.
CC -1- SUBUNIT: INTERACTS WITH CFLAR.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, EXCEPT
CC FOR PERIPHERAL BLOOD MONONUCLEAR LEUCOCYTES.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
CC -1- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR EMBL; U24231; AAA6517.1; .
 DR EMBL; X84709; CAA59197.1; .
 DR EMBL; BC000334; AAH00334.1; .
 DR PDB; 1ALW; 16-FEB-99.
 DR PDB; 1ALZ; 16-FEB-99.
 DR MIM; 602457; .
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 DR Apoptosis; 3D-structure.
 DR DOMAIN 3 81
 DR DOMAIN 97 181
 DR MUTAGEN 121 121
 DR CONFLICT 32 32
 DR SEQUENCE 208 AA; 23279 MW; 0E65E2F852E83507 CRC64;
 V->N: NO INTERACTION WITH FAS RECEPTOR.
 G -> V (IN REF 2).

Query Match 79.9%; Score 1040; DB 1; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.2e-74;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 49 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRLVRSVOSGLDLSMLEQNDLEPGHT 108
 Db 1 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRLVRSVOSGLDLSMLEQNDLEPGHT 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 168
 Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 120
 QY 169 VSDTKIDSTEDYPRNLTERVRSRLIRKNTKENATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTEDYPRNLTERVRSRLIRKNTKENATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 Db 181 QOARDLQNRSGAMSPMSWNSDASTSEAS 208

RESULT 2
 ID FADD_MOUSE STANDARD; PRT; 205 AA.
 AC Q61160; Q61082;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE FADD protein (FAS-associated death domain-containing protein)
 DE FADD protein (FAS-associated death domain-containing protein)
 GN FADD OR MOR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96220459; PubMed-8649383;
 RA Zhang J., Winoto A.;
 RT "A mouse Fas-associated protein with homology to the human Mort1/FADD
 RL protein is essential for Fas-induced apoptosis.";
 Mol. Cell. Biol. 16:2756-2763(1996).

RN SEQUENCE FROM N.A.
 RP MEDLINE-96152659; PubMed-8565075;
 RX Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
 RA "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
 RL receptor 1 signal transduction pathways.";
 RT Cell 84:299-308(1996).
 CC -|- FUNCTION: APOPTOTIC ADAPTOR MOLECULE THAT RECRUITS CASPASE-8 OR
 CC CASPASE-10 TO THE ACTIVATED FAS (CD95) OR TNFR-1 RECEPTORS. THE
 CC RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX
 CC (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8
 CC INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC
 CC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -|- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF THE
 CC CORRESPONDING DOMAIN WITHIN FAS RECEPTOR.
 CC -|- SIMILARITY: CONTAINS 1 DEATH EFFECTOR DOMAIN (DED).
 CC -|- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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DR EMBL; U50406; AAB07789.1; .
 DR EMBL; U43184; AAA97876.1; .
 DR HSSP; Q13158; 1A1Z.
 DR MGD; MGI:109324; Fadd.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50168; DED; 1.
 DR Apoptosis.
 DR DOMAIN 3 81
 DR DOMAIN 97 181
 DR CONFLICT 168 168
 DR SEQUENCE 205 AA; 22960 MW; 4BC8D86B33A58783 CRC64;
 C -> F (IN REF 2).

Query Match 55.3%; Score 719.5; DB 1; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.4e-49;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRLVRSVOSGLDLSMLEQNDLEPGHT 108
 Db 1 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRLVRSVOSGLDLSMLEQNDLEPGHT 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 168
 Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDVGKDWRRRLARQLK 120
 QY 169 VSDTKIDSTEDYPRNLTERVRSRLIRKNTKENATVAHLVGLRSCOMNLVADLVQEV 228
 Db 121 VSDTKIDSTEDYPRNLTERVRSRLIRKNTKENATVAHLVGLRSCOMNLVADLVQEV 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSE 254
 Db 181 QES---VSKSENNSPVLKRDSTVSSSE 203

RESULT 3
 ID ICE8_HUMAN STANDARD; PRT; 479 AA.
 AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;
 AC Q15806; Q90081; Q14676;
 DT 01-NOV-1997 (Rel. 35, Created)
 RN NCBI_TaxID=10090;
 [1]

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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:30:20 ; Search time 16.21 Seconds
(without alignments)
385.747 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VNOAECRFGGILGPLGKR.....RSGAMSPMSWNSDASTSEAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1302	100.0	256	5	PCT-US95-16542-2
2	1302	100.0	256	5	PCT-US96-10521-2
3	1047	80.4	208	1	US-08-618-164-3
4	1040	79.9	208	4	US-09-074-044A-19
5	1033	79.3	208	4	US-09-382-155-19
6	1028	79.0	208	4	US-09-064-414-6
7	985.5	75.7	201	4	US-09-064-414-4
8	982.5	75.5	201	4	US-09-064-414-2
9	438	33.6	85	4	US-09-042-785A-28
10	405	31.1	84	1	US-08-665-220-64
11	405	31.1	84	4	US-09-291-692-64
12	401	30.8	83	4	US-09-382-155-15
13	401	30.8	83	4	US-09-074-044A-15
14	382	29.3	74	4	US-08-995-159-5
15	318	24.4	62	4	US-08-894-626-5
16	128.5	9.9	250	4	US-09-187-789-48
17	122	9.4	180	4	US-09-382-155-18
18	122	9.4	180	4	US-08-807-200-2
19	122	9.4	220	2	US-09-074-044A-18
20	122	9.4	220	4	US-09-001-777-2
21	122	9.4	235	5	PCT-US96-10521-5
22	122	9.4	257	1	US-08-618-164-2
23	122	9.4	261	5	PCT-US96-10521-25
24	122	9.4	277	5	PCT-US96-10521-8
25	122	9.4	464	5	PCT-US96-10521-18
26	122	9.4	479	2	US-08-807-200-12
27	122	9.4	479	3	US-08-852-782-3

28	122	9.4	479	4	US-09-001-777-12	Sequence 12, Appl
29	122	9.4	479	5	PCT-US96-10521-7	Sequence 7, Appl
30	119	9.1	709	1	US-08-444-005-17	Sequence 17, Appl
31	117	9.0	75	4	US-09-291-692-66	Sequence 66, Appl
32	117	9.0	479	4	US-09-382-155-27	Sequence 27, Appl
33	117	9.0	479	4	US-09-382-155-28	Sequence 28, Appl
34	117	9.0	479	4	US-09-074-044A-27	Sequence 27, Appl
35	117	9.0	479	4	US-09-074-044A-28	Sequence 28, Appl
36	116	8.9	75	1	US-08-665-220-66	Sequence 66, Appl
37	116	8.9	81	2	US-08-807-200-4	Sequence 4, Appl
38	116	8.9	81	4	US-09-001-777-4	Sequence 4, Appl
39	116	8.9	83	4	US-09-382-155-11	Sequence 11, Appl
40	116	8.9	83	4	US-09-074-044A-11	Sequence 11, Appl
41	116	8.9	496	1	US-08-665-220-4	Sequence 4, Appl
42	116	8.9	496	1	US-09-291-692-4	Sequence 4, Appl
43	115.5	8.9	656	1	US-08-444-005-15	Sequence 15, Appl
44	115.5	8.9	656	1	US-09-069-023-28	Sequence 28, Appl
45	114	8.8	479	4	US-09-382-155-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
PCT-US95-16542-2
; Sequence 2, Application PC/TUS9516542
; GENERAL INFORMATION:
; APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
; APPLICANT: WEINMURZEL, Henry
; APPLICANT: WALLACH, David
; APPLICANT: BOLDIN, Mark
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: METT, Igor
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOL
; NUMBER OF SEQUENCES: 2
; NUMBER OF INVENTION: RECEPTORS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16542
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112022
; FILING DATE: 15-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112692
; FILING DATE: 19-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114615
; FILING DATE: 16-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16542-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-132;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQAPECFRGGGILGPKRRDLARASEPRTGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
Db 1 VQAPECFRGGGILGPKRRDLARASEPRTGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
QY 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
Db 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
Db 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
QY 181 YPRNLTERVRESLRWKNTKENATVAHLVGLARSCOMNLVADLVOEQVQARDLQNRSGA 240
Db 181 YPRNLTERVRESLRWKNTKENATVAHLVGLARSCOMNLVADLVOEQVQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
Db 241 MSPMSWNSDASTSEAS 256

RESULT 2
PCT-US96-10521-2
; Sequence 2, Application PC/TUS9610521
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: BRAXTON, SCOTT MICHAEL
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,615
; FILING DATE: 16-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,986
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 115,319
; FILING DATE: 14-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 116,588
; FILING DATE: 27-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 16-APR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10521-2

Query Match 100.0%; Score 1302; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.2e-132;

Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VQAPECFRGGGILGPKRRDLARASEPRTGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
Db 1 VQAPECFRGGGILGPKRRDLARASEPRTGARRAGPQPRPLADPAMPDFVLVLLHSVS 60
QY 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
Db 61 SSLSSSELTELKFLCLGRVVKRLKLVQSGDLFSLMLEQNDLEPGHTELLRELLASLRR 120
QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
Db 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNGKDWRRRLARQLKVSOTKIDSIEDR 180
QY 181 YPRNLTERVRESLRWKNTKENATVAHLVGLARSCOMNLVADLVOEQVQARDLQNRSGA 240
Db 181 YPRNLTERVRESLRWKNTKENATVAHLVGLARSCOMNLVADLVOEQVQARDLQNRSGA 240
QY 241 MSPMSWNSDASTSEAS 256
Db 241 MSPMSWNSDASTSEAS 256

RESULT 3
US-08-618-164-3
; Sequence 3, Application US/08618164
; Patent No. 5712115
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: BRAXTON, SCOTT MICHAEL
; TITLE OF INVENTION: HUMAN CELL DEATH-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ VERSION 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,164
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0058 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 791038
US-08-618-164-3

Query Match 80.4%; Score 1047; DB 1; Length 208;

	Best Local Similarity	100.0%;	Pred. No. 9.9e-105;		
	Matches	208;	Conservative	0;	Mismatches
				0;	Indels
				0;	Gaps
QY	49	MDPFLVLLHSVSSSSSELTKFLCLGRVYVKRLERVQSGLDLFSMLLEQNDLEPGHT	108		
Db	1	MDPFLVLLHSVSSSSSELTKFLCLGRVYVKRLERVQSGLDLFSMLLEQNDLEPGHT	60		
QY	109	ELLRELLASLRHDLRRVDDFEAGAAAGAAAGEEDLCAAFNVICDNVKGDKWRRLARQLK	168		
Db	61	ELLRELLASLRHDLRRVDDFEAGAAAGAAAGEEDLCAAFNVICDNVKGDKWRRLARQLK	120		
QY	169	VSDTKIDSTDYRPNLTERVRESLRINKNTEKENATVAHLGALRSCQMNLVADLVQEV	228		
Db	121	VSDTKIDSTDYRPNLTERVRESLRINKNTEKENATVAHLGALRSCQMNLVADLVQEV	180		
QY	229	QARQLNRSGAMSPMWSNDASTSEAS	256		
Db	181	QARQLNRSGAMSPMWSNDASTSEAS	208		

RESULT. 4
 US-09-074-044A-19
 ; Sequence 19, Application US/09074044A
 ; Patent No. 6207458
 ; GENERAL INFORMATION:
 ; APPLICANT: CHAUDHARY, PREET M
 ; APPLICANT: HOOD, LEROY
 ; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND
 ; TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOVER, WILLIAMS, TIMMONS & COLLINS
 ; STREET: 2405 GRAND BLVD., SUITE 400
 ; CITY: KANSAS CITY
 ; STATE: MISSOURI
 ; COUNTRY: USA
 ; ZIP: 64108
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/074,044A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COLLINS, JOHN M
 ; REGISTRATION NUMBER: 26,262
 ; REFERENCE/DOCKET NUMBER: 26588
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 816/474-9050
 ; TELEFAX: 816/474-9057
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 208 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 US-09-074-044A-19

Query Match	79.9%	Score 1040;	'DB 4';	Length 208;
Best Local Similarity	99.5%;	Prd.	No. 5.6e+104;	
Matches 207;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	49 MDPFVLLHVS	VSSLSSELTFLFCLGRVARKKRVQSGLDLFSMLLEQN	DLEPGHT	108
Db	1 MDPFVLLHVS	VSSLSSELTFLFCLGRVARKKRVQSGLDLFSMLLEQN	DLEPGHT	60

```

QY 109 ELLRELLASLRHHDLRRVDDFEAGAAAGAAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 168
Db 61 ELLRELLASLRHHDLRRVDDFEAGAAAGAAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 130
QY 169 VSDTKIDSIEDRYPRNLTERTVRESLRITWKNTKEKNATVAHLVGLALRSQCNMLVADLVQEV 228
Db 121 VSDTKIDSIEDRYPRNLTERTVRESLRITWKNTKEKNATVAHLVGLALRSQCNMLVADLVQEV 180
QY 229 QOARDLQNRGAMSPMSWNSDASTSEAS 356
Db 181 QOARDLQNRGAMSPMSWNSDASTSEAS 208

RESULT 5
US-09-382-155-19
; Sequence 19, Application US/09382155B
; Patent No. 6160095
; GENERAL INFORMATION:
; APPLICANT: CHAUDHARY, PREET M
; APPLICANT: HOOD, LEROY
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS
; TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
; FILE REFERENCE: Chaudhary
; CURRENT APPLICATION NUMBER: US/09/382,155B
; CURRENT FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 09/074,044
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-155-19

```

[illegible]

RESULT 6
US-09-064-414-6
: Sequence 6, Application US/09064414
: Patent No. 6248875
: GENERAL INFORMATION:
: APPLICANT: Wood, Andrew T
: APPLICANT: Bingham, Brendan W
: APPLICANT: Young, Kathleen H
: APPLICANT: Birsa, Camella
: TITLE OF INVENTION: Neuronal MORT1 Isoforms
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Andrea C. Walsh
: STREET: One Campus Drive
: CITY: Parsippany
: STATE: New Jersey

COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-6

Query Match 79.0%; Score 1028; DB 4; Length 208;
Best Local Similarity 98.6%; Pred. No. 1.1e-102;
Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 61 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 120
QY 169 VSDTKIDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQNNLVADLVQEV 228
Db 121 VSDTKIDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQNNLVADLVQEV 180
QY 229 QOARDLQNRSCAMSPMSWNSDASTSEAS 256
Db 181 QOARDLQNRSCAMSPMSWNSDASTSEAS 208

RESULT 7
US-09-064-414-4
Sequence 4, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal Mortl Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-064-414-4

Query Match 75.7%; Score 985.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 3.9e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCGRVVKRLERVQSGDLFSMLLEQNDLEPGHT 108
QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 58 ----ELLASLRHDLRRVDDFEAGAAAGAPGEDLCAAFNVICDNGKDWRRRLARQLK 113
QY 169 VSDTKIDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQNNLVADLVQEV 228
Db 114 VSDTKIDIEDYPRNLTERVRESLRWKTEKENATVAHLVGLRSCQNNLVADLVQEV 173
QY 229 QOARDLQNRSCAMSPMSWNSDASTSEAS 256
Db 174 QOARDLQNRSCAMSPMSWNSDASTSEAS 201

RESULT 8
US-09-064-414-2
Sequence 2, Application US/09064414
Patent No. 6248875
GENERAL INFORMATION:
APPLICANT: Wood, Andrew T
APPLICANT: Bingham, Brendan W
APPLICANT: Young, Kathleen H
APPLICANT: Birsan, Camelia
TITLE OF INVENTION: Neuronal Mortl Isoforms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrea C. Walsh
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,414
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: AHP-97147
TELEPHONE: (973) 683-2169
TELEFAX: (973) 683-4117

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 201 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-064-414-2

Query Match 75.5%; Score 982.5; DB 4; Length 201;
Best Local Similarity 95.7%; Pred. No. 8.1e-98;
Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCLGRVVKRLERVQSGDLFLSMLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCLGRVVKRLERVQSGDLFLSMLEQNDLEPGHT 57
QY 109 ELLRELLASRLRRHDLRRVDDFEAGAAAGAPCEEDLCAAFNVICDNGKDWRRRLARQLK 168
Db 58 ----ELLASRLRRHDLRRVDDFEAGAAAGAPCEEDLCAAFNVICDNGKDWRRRLARQLK 113
QY 169 VSDTKIDSTEDRYPRNLTERVRESLRINKNTEKENATVAHLVGLRSCQMNVLVADLVQEV 228
Db 114 VSDTKIDSTEDRYPRNLTERVRESLRINKNTEKENATVAHLVGLRSCQMNVLVADLVQEV 173
QY 229 QQARDLQNRSGAMPMSWNSDASTSEAS 256
Db 174 QQARDLQNRSGAMPMSWNSDASTSEAS 201

RESULT 9
US-09-042-785A-28
; Sequence 28, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandregouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELEPHONE: (617)742-4214
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 85 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-28

Query Match 33.6%; Score 438; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.7e-40;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 LCAAFNVICDNGKDWRRRLARQLKVSQTKIDSTEDRYPRNLTERVRESLRINKNTEKENA 204
Db 1 LCAAFNVICDNGKDWRRRLARQLKVSQTKIDSTEDRYPRNLTERVRESLRINKNTEKENA 60
QY 205 TVAHLVGLRSCQMNVLVADLVQEVQ 229
Db 61 TVAHLVGLRSCQMNVLVADLVQEVQ 85
RESULT 10
US-08-665-220-64
; Sequence 64, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note= "human FADD"
US-08-665-220-64

Query Match 31.1%; Score 405; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.7e-36;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 49 MDPFLVLLHSVSSSSSELTEKFLCLGRVVKRLERVQSGDLFLSMLEQNDLEPGHT 108
Db 1 MDPFLVLLHSVSSSSSELTEKFLCLGRVVKRLERVQSGDLFLSMLEQNDLEPGHT 60

RESULT	12
--------	----

US-09-074-044A-15

Query Match 30.8%; Score 401; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 7.1e-36;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHVSYSLSSELTEKFCICLRVVRKRLERVQSGLDLFSMLLEQNDLEPGHT 108
|||||
Db 1 MDPFLVLLHVSYSLSSELTEKFCICLRVVRKRLERVQSGLDLFSMLLEQNDLEPGHT 60
|||||

QY 109 ELLRELLASLRHDLRRVDDFE 131
|||||
Db 61 ELLRELLASLRHDLRRVDDFE 83
|||||

RESULT 14
US-08-995-159-5
; Sequence 5, Application US/08995159
; Patent No. 6130079
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995.159
FILING DATE: Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033.868
FILING DATE: 20-DEC-1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.0860001
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-995-159-5

Query Match 29.3%; Score 382; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.6e-34;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 ICDNVGKDWRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVG 211
|||||
Db 1 ICDNVGKDWRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVG 60
|||||

QY 212 ALRSCQNNLVADLV 225
|||||
Db 61 ALRSCQNNLVADLV 74
|||||

RESULT 15
US-08-894-626-5
; Sequence 5, Application US/08894626
; Patent No. 6355780
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BOLDIN, Mark P.
; VARFOLOMEEV, Eugene E.
; PANCER, Zeev
; METT, Igor
; GONCHAROV, Tanya M.
; WEINMURZEL, Henry

TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894.626
FILING DATE: 09-Dec-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 15-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-894-626-5

Query Match 24.4%; Score 318; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 WRRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVGALRSCQNN 219
|||||
Db 1 WRRLARQLKVSOTKIDSIEDRYPRNLTERVRESLRWKTKENATVAHLVGALRSCQNN 60
|||||

QY 220 LV 221
||
Db 61 LV 62
||

Search completed: August 17, 2002, 00:37:45
Job time: 445 sec

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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:34:15 ; Search time 69.07 seconds
(without alignments)
641.186 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VQAPFRCRGGILGLGKRR.....RSGAMSPWNSDASTSPAS 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131.5	10.1	482	11 Q9JHX4	Q9JHX4 rattus norv
2	128.5	9.9	476	13 Q918J3	Q918J3 brachydanio
3	125.5	9.6	480	11 Q89110	Q89110 m caspase 8
4	123.5	9.4	239	5 Q9V3B4	Q9V3B4 drosophila
5	122	9.4	276	4 Q96722	Q96722 homo sapien
6	121.5	9.3	1856	4 Q99407	Q99407 homo sapien
7	118.5	9.1	1719	4 Q13768	Q13768 homo sapien
8	118	9.1	941	11 Q61328	Q61328 rattus norv
9	117.5	9.0	1848	11 Q61302	Q61302 mus musculu
10	116.5	8.9	1975	5 Q9VCD1	Q9VCD1 drosophila
11	116	8.9	496	4 Q9COK4	Q9COK4 homo sapien
12	111	8.5	482	13 Q9OWU1	Q9OWU1 gallus gall
13	110	8.4	462	4 Q96TE4	Q96TE4 homo sapien
14	109	8.4	520	13 Q91B62	Q91B62 xenopus lae
15	103.5	7.9	461	5 Q96407	Q96407 lltomosoida
16	103.5	7.9	970	5 Q17342	Q17342 caenorhabdi

17	103.5	7.9	985	5	Q17341	Q17341 caenorhabdi
18	103.5	7.9	1786	5	Q17344	Q17344 caenorhabdi
19	103	7.9	1809	5	Q17487	Q17487 caenorhabdi
20	103	7.9	1815	5	Q17488	Q17488 caenorhabdi
21	103	7.9	1867	5	Q17486	Q17486 caenorhabdi
22	103	7.9	2039	5	Q17489	Q17489 caenorhabdi
23	103	7.9	6994	5	Q17343	Q17343 caenorhabdi
24	101.5	7.8	500	13	Q91B64	Q91B64 xenopus lae
25	100	7.7	2091	5	Q9VJ59	Q9VJ59 drosophila
26	99.5	7.6	218	11	Q99M25	Q99M25 rattus norv
27	99	7.6	919	16	Q9HZA6	Q9HZA6 pseudomonas
28	99	7.6	927	2	Q87015	Q87015 pseudomonas
29	99	7.6	1955	5	Q61308	Q61308 parascaris
30	98	7.5	381	11	Q9Q2M4	Q9Q2M4 mus musculu
31	98	7.5	472	10	Q943N5	Q943N5 oryza sativ
32	97	7.5	487	5	Q9GNM2	Q9GNM2 styela clav
33	97	7.5	622	17	Q9HQ32	Q9HQ32 halobacteri
34	97	7.5	665	4	Q96M89	Q96M89 homo sapien
35	96.5	7.4	1162	10	Q9LY65	Q9LY65 arabidopsis
36	96	7.4	647	16	Q9HUB1	Q9HUB1 pseudomonas
37	95.5	7.3	509	16	Q9A2N4	Q9A2N4 caulobacter
38	95.5	7.3	751	5	Q9NK92	Q9NK92 drosophila
39	95	7.3	406	16	P95251	P95251 mycobacteri
40	95	7.3	414	2	Q9XAF3	Q9XAF3 streptomyce
41	94.5	7.3	333	4	Q9NF94	Q9NF94 homo sapien
42	94.5	7.3	357	13	Q9DF34	Q9DF34 brachydanio
43	94	7.2	222	10	Q9SELS	Q9SELS arabidopsis
44	94	7.2	977	4	Q75300	Q75300 homo sapien
45	94	7.2	977	4	Q9H476	Q9H476 homo sapien

ALIGNMENTS

RESULT 1

Q9JHX4 ID Q9JHX4 PRELIMINARY; PRT; 482 AA.

AC Q9JHX4

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE CASPASE-8.

GN CASP8.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;

RA Cao G., Graham S.H., Chen D., Chen J.;

RT "Molecular cloning and characterization of rat caspase-8: Its

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF2793308; AAF87778.1;

DR EMBL; AF289372; AAK83055.1;

DR HSSP; Q15806; 10DU;

DR MEROPS; C14.009;

DR InterPro; IPR003576; Caspase.

DR InterPro; IPR001875; DED.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; IL1Bconv_enz.

DR Pfam; PF01335; DED; 2.

DR Pfam; PF00655; ICE_p10; 1.

DR Pfam; PF00656; ICE_p20; 1.

DR PRINTS; PR00376; IL1BCENZME.

DR SMART; SM00115; CASc; 1.

DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 DR PROSITE; PS0168; DED; 2.
 SQ SEQUENCE 482 AA; 55339 MW; 82BA429330C53264 CRC64;

Query Match 10.1%; Score 131.5; DB 11; Length 482;
 Best Local Similarity 40.5%; Pred. No. 0.0062;
 Matches 32; Conservative 12; Mismatches 34; Indels 1; Gaps 1;

OY 49 MDPFLVLLHVSLSSELTELKFLGRVVKRLRVOSGLDLFSMLLEQNDLPFGHT 108
 DB 1 MD-FHSLCYDIAERLGNELAAKFLCLDHIPQKQESINDVLVLFQRLQEGMLEEDNL 59
 OY 109 ELLRELLASLRHDLRRV 127
 DB 60 SFLKELLFHISRDLRSRV 78

RESULT 2
 Q918J3 ID Q918J3 PRELIMINARY; PRT; 476 AA.
 AC Q918J3
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15; Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE CASPASE-8.
 GN CASP8.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish";
 RL Cell Death Differ. 7:509-510(2000).
 DR EMBL; AF273220; AAF79207.1; -;
 DR HSP; Q15806; IQDU.
 DR MEROPS; C14.009; -;
 DR InterPro; IPR003576; Caspase.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002138; ICE-p10.
 DR InterPro; IPR001309; ICE-p20.
 DR InterPro; IPR002398; IL1Bconv_enz.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00655; ICE_p10; 1.
 DR Pfam; PF00656; ICE_p20; 1.
 DR PRINTS; PR00376; IL1BENZYM.
 DR SMART; SM00115; CASC; 1.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.
 DR PROSITE; PS0208; CASPASE_P20; 1.
 DR PROSITE; PS0168; DED; 2.
 SQ SEQUENCE 476 AA; 54950 MW; FD9DFE4B3C3C1FB9 CRC64;

Query Match 9.9%; Score 128.5; DB 13; Length 476;
 Best Local Similarity 28.1%; Pred. No. 0.011;
 Matches 59; Conservative 26; Mismatches 83; Indels 39; Gaps 10;

OY 49 MDPFLVLLHVSLSSELTELKFLGRVVKRLRVOSGLDLFSMLLEQNDLPFGHT 108
 DB 1 MDP--QIPHEIDENLTSGVDLAFCLDFIPKRRLESVTDKADKLRLDLQEGGLE--D 55
 OY 109 ELLRELLASLRHDLRRVDFEAGAAAGAPGEEDLCAAFNVICDNYGKD---WRLLA 164

Db 56 ELLPELLIAIGRIDLLEILKSKKEV-----ENL-----LRCDNRKGVSAIRKML 103
 OY 165 ROLKVSPTKIDSDIEDY-----PRNTERVRESLRWKNTKENA-----TVAHLVG 211
 Db 104 --LKISE--DMTEENFRAKFLDLPRAKLGRTSFLDALIEMEKQORLPDNLDELVR 158
 OY 212 ALRSCONNLVADLVQEQVQARDLQNRSGAM 241
 Db 159 ILEKCDKQLAVMIERFRNQRSHRDQEGGRL 188

RESULT 3
 O89110 ID O89110 PRELIMINARY; PRT; 480 AA.
 AC O89110; O35669;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE CASPASE 8 PRECURSOR (EC 3.4.22.-) (CASPASE-8) (ICE-LIKE APOPTOTIC
 DE ICE/CED-3-LIKE PROTEASE) (FADD-ASSOCIATED CED-3 HOMOLOG) (MACH) (FADD-HOMOLOGOUS
 DE PROTEASE) (APOPTOTIC PROTEASE MCH-5) (CAP4).
 GN CASP8 OR CASP-8 OR FLICE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=129/SVJ;
 RA MEDLINE=98316661; PubMed=9654089;
 RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
 RT "Molecular cloning and characterization of mouse caspase-8";
 RL Eur. J. Biochem. 253:399-405(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC MEDLINE=99057979; PubMed=9837723;
 RA Van de Craen M., Van Loo G., Declercq W., Schotte P.,
 RA van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W.,
 RA Vandenabeele P.;
 RT "Molecular cloning and identification of murine caspase-8";
 RL J. Mol. Biol. 284:1017-1026(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 57-476 FROM N.A.
 RA Kioschis P., Kischkel F., Poustka A., Kramer P.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND
 CC TNFR-1 INDUCED CELL DEATH. BINDING TO THE ADAPTER MOLECULE FADD
 CC RECRUITS IT TO EITHER RECEPTOR. THE RESULTING AGGREGATE CALLED THE
 CC DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN
 CC LIBERATED FROM THE DISC AND ACTIVATES DOWNSTREAM APOPTOTIC
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE
 CC (CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND
 CC ACTIVATES CASPASE-1, -2, -3, -6, -7, -8, -11/4 AND -12.
 CC -1- FUNCTION: MAY PARTICIPATE IN THE GRANYME B APOPTOTIC PATHWAYS.
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP).
 CC HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-|-AMC
 CC (BY SIMILARITY).
 CC -1- ENZYME REGULATION: INHIBITED BY Z-VAD-FK, CRMA AND P35.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC HIGHEST EXPRESSION IN SPLEEN, THYMUS, LUNG, LIVER AND KIDNEY.
 CC LOWER EXPRESSION IN HEART, BRAIN, TESTIS AND SKELETAL MUSCLE.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST EXPRESSION OCCURS AT
 CC DAY 7.
 CC -1- DOMAIN: CONTAINS TWO DEATH EFFECTOR DOMAINS (ALSO CALLED MORT
 CC MODULES) WHICH ARE INVOLVED IN THE BINDING OF CORRESPONDING

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CC CC      SEQUENCE MOTIFS WITHIN FADD PROTEIN.
CC CC      -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC
CC CC      WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC
CC CC      ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND CASPASE-10 CAN
CC CC      BE INVOLVED IN THESE PROCESSING EVENTS (BY SIMILARITY).
CC CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14; ALSO KNOWN AS THE
CC CC      CASPASE FAMILY.
DR EMBL; AF067841; AAC40132.1; -
DR EMBL; AF067835; AAC40132.1; JOINED.
DR EMBL; AF067836; AAC40132.1; JOINED.
DR EMBL; AF067837; AAC40132.1; JOINED.
DR EMBL; AF067838; AAC40132.1; JOINED.
DR EMBL; AF067839; AAC40132.1; JOINED.
DR EMBL; AF067840; AAC40132.1; JOINED.
DR EMBL; AF067834; AAC40131.1; -
DR EMBL; AJ007749; CAA07677.1; -
DR EMBL; BC006641; CAA04196.1; -
DR EMBL; AC006737; AAH06737.1; -
DR HSP; Q15806; 1000.
DR MEROPS; C14.009; -
DR MG; MG1:1261423; Casp8.
DR InterPro; IPR003576; Caspase.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF01335; DED; 2.
DR Pfam; PF00855; ICE_P10; 1.
DR Pfam; PF00856; ICE_P20; 1.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS01668; DED; 2.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 218 BY SIMILARITY.
FT CHAIN 219 376 CASPASE-8 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 377 387 BY SIMILARITY.
FT CHAIN 388 480 CASPASE-8 SUBUNIT P10 (BY SIMILARITY).
FT ACT_SITE 319 319 BY SIMILARITY.
FT ACT_SITE 362 362 BY SIMILARITY.
FT DOMAIN 3 80 DEATH EFFECTOR DOMAIN (BY SIMILARITY).
FT DOMAIN 101 177 DEATH EFFECTOR DOMAIN (BY SIMILARITY).
FT CONFLICT 68 71 HISR -> PHPVG (IN REF. 4).
FT CONFLICT 94 99 DNQIS -> RQCPRL (IN REF. 4).
FT CONFLICT 96 96 A -> V (IN REF. 2).
FT CONFLICT 103 107 VMLFK -> SCSEF (IN REF. 4).
FT CONFLICT 475 475 K -> N (IN REF. 4).
SQ SEQUENCE 480 AA; 55356 MW; 045268AE3DE5ED4F CRC64;

Query Match 9.6%; Score 125.5; DB 11; Length 480;
Best Local Similarity 39.5%; Pred. No. 0.02;
Matches 30; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 49 MDPEVLVHVSLSSELTETLFCGLGRVVRKRLRVQSLDLSMLENDLLEPGHT 108
Db 1 MD-FQSCLYAIAEELGSEDLAALKFLCLDLYPHKQETIEDAKFLRLRKNLEGNL 59

Qy 109 ELLRELLASLRHRLDL 124
Db 60 SFLKELLFHSRWDL 75

RESULT 4
Q9V3B4 ID Q9V3B4 PRELIMINARY; PRT; 239 AA.
AC Q9V3B4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG12297 PROTEIN (DEATH DOMAIN-CONTAINING ADAPTOR PROTEIN).

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GN BG4 OR CG12297.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer E.G., Heit G., Champs M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., An H.-J., Nelson C.R., Miklos G.L.G.,
RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Belcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Flosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou L., Steller H.;
RT "BG4, a potential Drosophila homologue of FAS-associating death-domain
RT containing protein (FADD).";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469420; Pubmed=10934188;
RA Hu S., Yang X.;
RT "FADD, a Novel Death Domain-containing Adapter Protein for the
RT Drosophila Caspase DREDD.";
RL J. Biol. Chem. 275:30761-30764(2000).
DR EMBL; AE003737; AAF55950.1; -
DR EMBL; AF222005; AAF44325.1; -
DR EMBL; AF295103; AAG22535.1; -
DR FlyBase; FBgn0038928; BG4.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; death; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
SQ SEQUENCE 239 AA; 27421 MW; F43CFAA546C3FCD9 CRC64;

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Query Match

9.4%; Score 122.5; DB 5; Length 239;

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Best Local Similarity 20.8%; Pred. No. 0.014;
Matches 46; Conservative 44; Mismatches 70; Indels 61; Gaps 7;

Qy 65 SSELTELKFLCGRV-VKKLRLVQSGDLDFSMLEQNDLEPGHTELLASLRR--- 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
21 TENVEOLKLFVEEIGSRSSDCITIEDLDCLERADELSEYNVEPLRRISGNPOLIE 80
Qy 121 -----HDLRRVDDFE-----AGAAAGAAPEEDICAA----- 148
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
81 ALSATKPNILGHPVNYQELRAELQRLRIAPASQNAQPSVSELAAPPTATQNY 140
Qy 149 -----FNVICDNGVDKWRRLARQLKVDTKIDSIEDRYPRNLTERVRESLR 194
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 ATPAAFTDHRKRWFKKISEELGRWRRLGRSAGISGQMDTIERYPHDLKSOI---LR 197
Qy 195 INKTEKENA-----TVAHVGLARSCOMLVADLVEVQO 230
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
198 LLQLEEDDCHDPKHFLRLRLCRLGDCGRN---DLRRRVEQ 235

RESULT 5
Q96T22 PRELIMINARY; PRT; 276 AA.
ID AC Q96T22;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CASPASE-8L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RA Himeji D., Tsukamoto H., Horiuchi T.;
RT "A novel isoform of caspase-8 (caspase-8L) is an endogenous inhibitor
RT of apoptosis.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC380342; AAK57437.1;
SQ SEQUENCE 276 AA; 32330 MW; 227ED7718788F92 CRC64;

Query Match
Best Local Similarity 9.4%; Score 122; DB 4; Length 276;
Matches 38; Conservative 23; Mismatches 55; Indels 16; Gaps 4;

Qy 56 LHSVSSLSSELTELKFLCGRVVKRLVQSGDLDFSMLEQNDLEPGHTELLRELL 115
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
7 LYDIGQLDSEDLASLKFSLDYIPORQEPKIDALMLFQRLQEKRLSESNLSFLKELL 66
Qy 116 ASLRRHDL-----RVDDFEAGAAGAAPEEDICAAFNVICDNGVDKWR---L 163
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 FRINRLDLITLNTKEMEREL---QTPGRAQI-SAYRVMLYQISEVSRSELRSFKF 122
Qy 164 ANQLKVDTKID 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 LLQEISRKCLD 134

RESULT 6
Q99407 PRELIMINARY; PRT; 1856 AA.
ID AC Q99407;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANKYRIN.
GN ANK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=97382244; PubMed=9235914;
RA Gallagher P.G., Tse W.T., Scarpa A.L., Lux S.E., Forget B.G.;
RT "Structure and organization of the human ankyrin-1 gene. Basis for
RT complexity of pre-mRNA processing.";
RL J. Biol. Chem. 272:19220-19228(1997).
DR EMBL; U50133; AAB47805.1; JOINED.
DR EMBL; U50092; AAB47805.1; JOINED.
DR EMBL; U50093; AAB47805.1; JOINED.
DR EMBL; U50094; AAB47805.1; JOINED.
DR EMBL; U50095; AAB47805.1; JOINED.
DR EMBL; U50096; AAB47805.1; JOINED.
DR EMBL; U50097; AAB47805.1; JOINED.
DR EMBL; U50098; AAB47805.1; JOINED.
DR EMBL; U50099; AAB47805.1; JOINED.
DR EMBL; U50100; AAB47805.1; JOINED.
DR EMBL; U50101; AAB47805.1; JOINED.
DR EMBL; U50102; AAB47805.1; JOINED.
DR EMBL; U50103; AAB47805.1; JOINED.
DR EMBL; U50104; AAB47805.1; JOINED.
DR EMBL; U50105; AAB47805.1; JOINED.
DR EMBL; U50106; AAB47805.1; JOINED.
DR EMBL; U50107; AAB47805.1; JOINED.
DR EMBL; U50108; AAB47805.1; JOINED.
DR EMBL; U50109; AAB47805.1; JOINED.
DR EMBL; U50110; AAB47805.1; JOINED.
DR EMBL; U50111; AAB47805.1; JOINED.
DR EMBL; U50112; AAB47805.1; JOINED.
DR EMBL; U50113; AAB47805.1; JOINED.
DR EMBL; U50114; AAB47805.1; JOINED.
DR EMBL; U50115; AAB47805.1; JOINED.
DR EMBL; U50116; AAB47805.1; JOINED.
DR EMBL; U50117; AAB47805.1; JOINED.
DR EMBL; U50118; AAB47805.1; JOINED.
DR EMBL; U50119; AAB47805.1; JOINED.
DR EMBL; U50120; AAB47805.1; JOINED.
DR EMBL; U50121; AAB47805.1; JOINED.
DR EMBL; U50122; AAB47805.1; JOINED.
DR EMBL; U50123; AAB47805.1; JOINED.
DR EMBL; U50124; AAB47805.1; JOINED.
DR EMBL; U50125; AAB47805.1; JOINED.
DR EMBL; U50126; AAB47805.1; JOINED.
DR EMBL; U50127; AAB47805.1; JOINED.
DR EMBL; U50128; AAB47805.1; JOINED.
DR EMBL; U50129; AAB47805.1; JOINED.
DR EMBL; U50130; AAB47805.1; JOINED.
DR EMBL; U50131; AAB47805.1; JOINED.
DR EMBL; U50132; AAB47805.1; JOINED.
DR HSP; Q00420; IAWC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 22.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00095; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS00088; ANK_REPEAT; 20.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1856 AA; 203466 MW; 4A4E3A794DD6401F CRC64;
```

```
Query Match
Best Local Similarity 9.3%; Score 121.5; DB 4; Length 1856;
Matches 34; Conservative 28; Mismatches 56; Indels 7; Gaps 2;

Qy 137 GAAPGEEDLCAAFNVICDNGVDKWRRLARQLKVDTKIDSIEDRYPRNLTERVRESLR 196
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1370 GSLSGTQAEKMKMAVISEHGLSLGSLAEQLQFSVEDINRVRNPNLSLEQSVALLNLW 1429
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QY 197 NTEKENATVAHLVGLRSCQMLNVLADLVQ-EVQQRDLQ-----NRSGAMSPMSWNSD 249
Db 1430 VIREGQNNANMENLYALQSDRGEIVNMLEGSGRQSNLKPDRRHRDTRDYSLSPSQMGY 1489
QY 250 ASTSE 254
Db 1490 SSLQD 1494

RESULT 7
Q13768 PRELIMINARY; PRT; 1719 AA.
AC Q13768;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE ALT. ANKYRIN (VARIANT 2.2).
DE ALT. ANKYRIN (VARIANT 2.2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEMATOPOIETIC;
RX MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT structure with homology to tissue-differentiation and cell-cycle
RT control proteins."
RL Nature 344:36-42(1990).
DR EMBL; X16609; CAA3461.1; -.
DR HSP; Q00420; 1AWC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 22.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1719 AA; 189011 MW; F63465D16D975CBF CRC64;

Query Match 9.1%; Score 118.5; DB 4; Length 1719;
Best Local Similarity 28.0%; Pred. No. 0.42;
Matches 33; Conservative 26; Mismatches 52; Indels 7; Gaps 2;

QY 137 GAARGEEDLCAAFNYCDNVGDKRRRLARQLKVSQDKTIDSDRYPRNLTRVRESLRW 196
Db 1395 GSLSGTEQAENKMAVISHLSLNAELARELQFVEDINRTRVENPSLLEQSVALLNLW 1454
QY 197 NTEKENATVAHLVGLRSCQMLNVLADLVQ-EVQQRDLQ-----NRSGAMSPMSWNSD 247
Db 1455 VIREGQNNANMENLYALQSDRGEIVNMLEGSGRQSNLKPDRRHRDTRDYSLSPSQMN 1512

RESULT 8
Q63128 PRELIMINARY; PRT; 941 AA.
AC Q63128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE CPG2 PROTEIN.
DE CPG2.
GN Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HIPPOCAMPAL DENTATE GYRUS;
RX MEDLINE=96312537; PubMed=8700863;
RA Nedivi E., Feldust S., Theill L., Hevroni D.;
RT "A set of genes expressed in response to light in the adult cerebral
RT cortex and regulated during development."
RL Proc. Natl. Acad. Sci. U.S.A. 93:2048-2053(1996).
DR EMBL; X95466; CAA64740.1; -.
DR InterPro; IPR002017; Spectrin.
SQ SEQUENCE 941 AA; 109037 MW; EC50B042E2AF4248 CRC64;

Query Match 9.1%; Score 118; DB 11; Length 941;
Best Local Similarity 22.7%; Pred. No. 0.21;
Matches 58; Conservative 47; Mismatches 96; Indels 54; Gaps 11;

QY 11 GGILGPLKRR-----DLARASEPRTGARRAGOPRPLADPAMPDFVLVLSVSSLS- 65
Db 678 GEILSWLKSRLKHLIDVSSNE-----AQRGDELAELSS-SFKALVALLSEVEKMLSNF 731
QY 66 SELTELKFLCLGRVVKRLERVQSG---LDLFSMLLEQNDLEPGHTELLRE-----LLAS 117
Db 732 GECVOYK-----EIVKSLGLEMSGSESKDEATITDENTLFAOQMLLRHQOKTKMIS 786
QY 118 LRRHDLRLRVDFAGAAAGAEEDLCAAFNYCDNVGDKRRRLARQLKVSQDKTIDSI 177
Db 787 AKRDLQOQMEQGGQGGQAG--PGQEEL-----RKLESTLTGLEOS 825
QY 178 EDRYPRNLTRVRESLRINKTEKENATVAHLV-----GALRSCQMLNVLADLVQEVQQR 232
Db 826 RERQER-----RIQVSLRKWERFETNKETVYVYLFQGTSSHERFLSFLSLESLSLE 881
QY 233 DLQNRSGAMSPMSWN 247
Db 882 EFSKRATESIATQAE 896

RESULT 9
Q61302 PRELIMINARY; PRT; 1848 AA.
AC Q61302;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ERYTHROID ANKYRIN.
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=NEURAL;
RX MEDLINE=93252825; PubMed=8486643;
RA Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RA Barker J.E.;
RT "Complex patterns of sequence variation and multiple 5' and 3' ends
RT are found among transcripts of the erythroid ankyrin gene."
RL J. Biol. Chem. 268:9533-9540(1993).
DR EMBL; X69063; CAA48801.1; -.
DR HSP; Q00420; 1AWC.
DR MGD; MGI:88024; Ank1.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 23.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.

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DR	SMART; SM00248; ANK; 22.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00218; ZUS; 1.
DR	PROSITE; PS50088; ANK_REPEAT
DR	PROSITE; PS50297; ANK_REPEAT
DR	PROSITE; PS50017; DEATH_DOMAIN
KW	ANK repeat; Repeat.
SQ	SEQUENCE 1848 AA; 2025

Query Match 9.0%; Score 117.5; DB 11; Length 1848;
Best Local Similarity 27.9%; Pred. NO. 0.56;
Matches 31; Conservative 29; Mismatches 44; Model 7

Qy	151	V	I	C	O	N	G	K	O	W	R	L	A	R	K	L	V	S	D	K	I	S	E	D	R	P	N	L	T	R	V	R	S	L	R	I	K	K	E	N	A	T	V	A	H	V		210	
Db	1421	V	I	R	E	H	L	G	S	A	E	L	A	R	K	E	S	I	I	R	I	V	E	N	P	N	S	L	D	S	T	A	L	L	I	W	D	R	E	G	E	N	A	K	M	E	N		1480
Qy	211	G	A	L	R	S	O	M	N	L	V	A	D	L	V	O	-	E	V	O	A	R	D	L	Q	-	-	-	-	-	N	R	S	G	A	M	P	M	S	W	N	S	D	A	S	T	E		254
Db	1481	T	A	L	N	I	D	R	E	I	V	N	M	L	E	G	R	S	O	N	L	K	P	E	R	R	I	G	D	R	E	I	S	L	S	Q	V	A	N	G	Y	S	L	Q		1531			

RESULT	10	
Q9VCD1		
ID	Q9VCD1	PRELIMINARY; PRT; 1975 AA.
AC	Q9VCD1	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE	CG6129 PROTEIN.	
GN	CG6129.	

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N. A.

RC STRAIN-BERKELEY;

MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.C., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G.G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Fogle C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K.C., Nusskern D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinart K., Sengen-Klamos I., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Sidon-Klamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Glabbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 RL EMBL: AE003746; AAF56238.1; -.
 FlyBase: FBgn0039152; CG6129.
 DR InterPro: IPR001871; bzip.
 DR SMART: SM00338; BRL2; 1.
 SQ SQUANCE 1975 AA; 224509 MW; 62BA92C10D3478CC CRC64

Query Watch	8.9%	Score 116.5:	DB 5:	Length 1975:
Best Local Similarity	23.5%	Pred. No. 0.74:		
Matches 66:	Conservative 45:	Mismatches 105:	Indels 65:	Gaps
QY	10	GGGILGPGKGRDRLARASEPRTEGARRAGPQRPPLADPAMDPLVLLHSSVSSLSSELT	69	
Db	479	GGGGKSP---RRNSTASQAFAECTISA-----VQAAHHKYQLALHDMQVKQNTSET	538	
QY	70	ELKFLCLGRVVKRLERVQSGDLDFSMLEQ--NDLEPGHTELLRELLASLRHHDLRRV	137	
Db	529	L-----RTTKAGLETSEGTKOLLTKKMOOLETKLDSSNSK-ISELQ---ERESLQGL	578	
QY	128	DPFEAGAAAGAPEEDLCAAFVVICDNYGKDWRRRLAROLKVSYOTKIDSTED-----	179	
Db	579	DDIRV-OKQOSEMGRADINSAF---ENLSSDYEKMQNLCKQLKRIDSDMEEDKAVELE	633	
QY	180	---RYPNLTF-----RVRE---SLRIKVN-----TKENATVAHLVGAL	213	
Db	634	IQRIKDKNTLNLRSDEDRSLREETISURLEENRVSLNROLLPOORTESDNINLL	693	
QY	214	RSCQNLVADLVQVQOQARDLQNRGAMSPMSWNSDASTSE	254	
Db	694	EKQKSDLEYLDLKKLLPKCQLOKQEKHKL-----NNSCSTSD	730	

RESULT 17

Q9COK4	PRELIMINARY;	PRT; 496 AA.
AC Q9COK4;		
DT 01-JUN-2001	(TREMBLrel. 17, Created)	
DT 01-JUN-2001	(TREMBLrel. 17, Last sequence update)	
DE 01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE CASPASE-8.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa;		
OC Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX NCBI_TaxID=9606;		
RN [1]		
RP SEQUENCE FROM N.A.		
RR MEDLINE=21100893; PubMed=11161814;		
RA Hadeno S., Yanggisawa Y., Skaug J., Fichter K., Nasir J.,		
RA Martindale D., Koop B.F., Scherer S.W., Rouleau G.A.,		
RA Ikeda J.-E., Hayden M.R.;		
RA "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,		
RT and ALS2CR3 in the juvenile amyotrophic lateral sclerosis (ALS2)		
RT critical region at chromosome 2q33-q34: Candidate genes for ALS2."		
RL Genomics 71:200-213(2001).		
DR EMBL; AB038985; BAB32555.1; -.		
DR EMBL; AB038982; BAB32555.1; JOINED.		
DR EMBL; AB038983; BAB32555.1; JOINED.		
DR EMBL; AB038984; BAB32555.1; JOINED.		
DR HSP; Q15806; IODU.		
DR InterPro; IPRO03576; Caspase.		
DR InterPro; IPRO01875; DED.		
DR InterPro; IPRO02138; ICE_p10.		
DR InterPro; IPRO01309; ICE_p20.		
DR InterPro; IPRO02398; ILIBconv enz.		
DR Pfam; PF01335; DED; 2.		
DR Pfam; PF00655; ICE_p10; 1.		
DR Pfam; PF00656; ICE_p20; 1.		

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DR PRINTS; PRO0376; ILIBCENZYME.
DR SMART; SM00115; CASC; 1.
DR SMART; SM00031; DED; 2.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS02007; CASPASE_P10; 1.
DR PROSITE; PS02008; CASPASE_P20; 1.
DR PROSITE; PS0168; DED; 2.
SQ SEQUENCE 496 AA; 57723 MW; 041C5E27E0E261AE CRC64;

Query Match      8.9%; Score 116; DB 4; Length 496;
Best Local Similarity 39.1%; Pred. No. 0.13;
Matches 27; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

QY 56 LHSVSSSSSELTELKFLCGRVYVKKLERSVQGLDLSMLLEQNDLSPGHTELLRELL 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LYDIGQLQSEDASLKFLSLDYIPORKQEPKDALMLFQKQKRMLESNLSFLKELL 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 ASLRHDL 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 FRINRLDLL 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
Q90WU1 PRELIMINARY; PRT; 482 AA.
ID Q90WU1
AC Q90WU1
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CASPASE 8.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057939; AAL23700.1;
SQ SEQUENCE 482 AA; 54645 MW; 8E39336B6E090BEF CRC64;

Query Match      8.5%; Score 111; DB 13; Length 482;
Best Local Similarity 25.4%; Pred. No. 0.33;
Matches 53; Conservative 28; Mismatches 84; Indels 44; Gaps 5;

QY 52 FLVLLHVSSSLSSELTELKFLCGRVYVKKLERSVQGLDLSMLLEQNDLSPGHTELL 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 FSQLLFVISEALDTELASLFLSLHVTVRKREDIEEPKAFQALQEKGMIEVGLDFEL 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 112 RELASLRHDLRRVDVDFEAGAAGAPGEDLCAAFNVICDVGKWRRLARQLKYSVD 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 KELLYRINRIDL-----ASYLSSREEMERELQVFGARVSPFRYLLFOLSENI 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 172 TKID-----SIEDRYPNLTERVRESLRINKTEKENATV-----LKEDNLVLTICKV 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 TKDDMKCFKFLGLKLPCKLSPTTMDVFEIEKKGI-----LKEDNLVLTICKV 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 207 -AHLVGALRSQMLNVLAD---LVQEVQQA 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 DKSLKKIEDYELNLLGEGEMLVTEGQRS 196
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RESULT 13
Q96TE4 PRELIMINARY; PRT; 462 AA.
ID Q96TE4
AC Q96TE4
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE USURPIN BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21100893; PubMed=11161814;
RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.;
RT "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2,
RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: Candidate genes for ALS2.";
RL Genomics 71:200-213(2001).
DR EMBL; AB038972; BAB32552.1;
DR EMBL; AB038967; BAB32552.1; JOINED.
DR EMBL; AB038968; BAB32552.1; JOINED.
DR EMBL; AB038969; BAB32552.1; JOINED.
DR EMBL; AB038970; BAB32552.1; JOINED.
DR EMBL; AB038971; BAB32552.1; JOINED.
SQ SEQUENCE 462 AA; 52550 MW; D4E0109CBA47EAA3 CRC64;

Query Match      8.4%; Score 110; DB 4; Length 462;
Best Local Similarity 25.9%; Pred. No. 0.38;
Matches 49; Conservative 29; Mismatches 93; Indels 18; Gaps 6;

QY 55 LLHSVSSLSSELTELKFLCGRVYVKKLERSVQGLDLSMLLEQNDLSPGHTELLRELL 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 VHQVEEALDTDEKEMLEFLCGRVYVPPNVR---DLLDLRERKLSVGD---LAEL 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 LASLRHDLRRVDVDFEAGAAGAPGEDLCAAFNVICDVGKWRRLARQLKYSVDK- 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 LYRVRRFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAEIGD-----LQKSDVSS 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 174 -IDSIEDRYPNLTERVRESLRINKTEKENATV-AHLVGALRSQMLN-VADLVQEVQQA 231
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Db 112 LIFLMKDYMGKISKESKSFLLDVLVELEKLNVLAPDQDLLEKCKNIHRIDLTKTKY 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 232 RDLQNRSGA 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 K-QSVOGA 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
Q9IB62 PRELIMINARY; PRT; 520 AA.
ID Q9IB62
AC Q9IB62
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CASPASE-10.
GN XCASPASE-10.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038173; BAA94751.1;
DR HSSP; Q15806; IQDU.
DR MEROPS; C14; UPW; -.
DR InterPro; IPR003576; Caspase.
DR InterPro; IPR001875; DED.
DR InterPro; IPR002138; ICE_p10.

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DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; ILIbconv_enz.
DR Pfam: PF01335; DED; 2.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILIbCENZYME.
DR SMART: SM00115; CASC; 1.
DR SMART: SM00031; DED; 2.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
DR PROSITE: PS0168; DED; 2.
SQ SEQUENCE 520 AA; 59626 MW; 33164A5A09CA6615 CRC64;

Query Match 8.4%; Score 109; DB 13; Length 520;
Best Local Similarity 25.6%; Pred. No. 0.54; Mismatches 89; Indels 30; Gaps 8;
Matches 53; Conservative 35; Mismatches 89; Indels 30; Gaps 8;
QY 49 MDPFVLLHSVSSLSSELTEKFLGRVYKRLERVOSGLDFSMLEQNDEPGHT 108
DB 1 MD-FNSMLLRIDIDGLGREDIEALKFLCRDVLKRNKLLSVQSGHELFOQLMTEDLINEDNY 59
QY 109 ELRLRELLASLRHDLRRV--DDFEAGAAA---GAAPGEEDLCRAFNVICDNV-CKDWR 161
DB 60 FLGLGELLYINHSLSLHDGTVKVEVQKALPHHWKISPYRQMLYE----LSENVGTGEDEK 115
QY 162 RLARQLKVSDTKIDSIEDRYPRNLTERVRESLRINWTEKENATVAHLVGLRSCOMNLV 221
DB 116 RLFLFIL-----PLKKHKENKT-----FLDVLQLEKENAITEEDNVKLLVEEVRKVS 162
QY 222 ADLVEVQVQARDLQNR-----SCAMSP 243
DB 163 PDLKTIERYKRGDKLHRPEIGLMQP 189

RESULT 15
O96407 PRELIMINARY; PRT; 461 AA.
AC O96407;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANKYRIN HOMOLOG (FRAGMENT).
GN E1.
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Domeyer A.N., Gallin M., Ertmann K.D.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF039830; AAC98928.1; -
DR InterPro: IPR00488; Death.
DR Pfam: PF00531; Death; 1.
DR SMART: SM00005; DEATH; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
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SQ SEQUENCE 461 AA; 52345 MW; 892364FB9872039A CRC64;

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Matches 32; Conservative 16; Mismatches 32; Indels 11; Gaps 4;
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DB 154 IGADWHRRLARALEVPDIDIROVRHQF---VGLEATILRIWRFLEKKEQTAPA----ALRS 206
QY 216 COMNLVA-DLVEVQVQAR---DLQNRSGAMS 242

DB 207 AFQRIGRDDVVREMNRAEKPDDEGTGTSVSIS 237
Search completed: August 17, 2002, 00:40:24
Job time: 369 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: August 17, 2002, 00:37:15 ; Search time 1697.03 seconds
(without alignments)
13528.530 Million cell updates/sec
Title: US-09-824-134-1
Perfect score: 1701
Sequence: 1 GTGAATCAGCAGCGAGTG.....ACAAAAA
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
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prime, mRNA linear EST 16-FEB-2001
ACCESSION
AL544558
VERSION
AL544558.1 GI:12877038
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1117)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 228 a 325 c 359 g 196 t 9 others
ORIGIN

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	1010.8	59.4	1117 9	AL544558	AL544558
2	999.2	58.7	1081 9	AL575812	AL575812
3	981	57.7	1034 9	AL528456	AL528456
4	973.6	57.2	1031 9	AL570642	AL570642
5	953.8	56.1	983 9	AL573044	AL573044
6	933.2	54.9	956 9	AL548504	AL548504
7	924	54.3	973 9	AL527771	AL527771
8	895.6	52.1	912 9	AL528496	AL528496
9	872.8	51.3	955 9	AL562839	AL562839
10	862.4	50.7	961 9	AL521788	AL521788
11	846	49.7	854 9	AL527192	AL527192
12	843.6	49.6	1038 9	AL575732	AL575732
13	827	48.6	922 9	AL518571	AL518571
14	826.2	48.6	859 9	AL556073	AL556073
15	812.6	47.8	859 9	AL517525	AL517525
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17	784.4	46.1	880 9	AL530790	AL530790

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QY 1294 GACACTAGGCTCAGCGGGGCTGCTGTGTGGGAGAGCATGGCTGGGGTGGGGTGGG 1353
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QY 1354 AGACCTGGTGGCCGTGTGACAGCTTTGGGCCCTGTGTGAGTTGAGTCTCTCTCTGAG 1413
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Db 300 GGRCCKGTTGGCSGTGTGCTGGGCTTTGGGCCCTGTGTGAGTTGAGTCTCTCTCTGAG 241
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QY 1414 ACTGCTAAGTAGGCGCAGTGATGTTGCCAGGAGCATGGCTGGGGTGGGGTGGGTCG 1473
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RESULT 3
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LOCUS AL528456 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC029YB02 3
DEFINITION prime, mRNA sequence.
ACCESSION AL528456
VERSION AL528456.1 GI:12791949
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .1034
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 239 a 295 c 269 g 224 t 7 others
ORIGIN
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Best Local Similarity 98.2%; Pred. No. 5.4e-157;
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Db 1033 CAACAGTGGCCCTGGTGGGGGTCTCAGGTCTCTGCCAGATGAACCTGGTGGCTGACC 974
|||||
QY 671 TGGTACAGAGGTTTACAGCAGCCCGTACCTCCAGAGAGAGTGGGCCATGTCCTCCGA 730
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Db 973 TGGTACAGAGGTTTACAGCAGCCCGTGMCCYCCAGMACAGAGTGGGCCATGTCCTCCGR 914
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QY 731 TGTATGGAATCAGAGCATCTACCTCCAGAGCGTCTCTGATGGCCGCTGCTTTGGCT 790
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Db 793 ACTGTGAAGACCCAGCAGGAGCCAGGCTGAGTGAGCCACAGACACCTGCTTCTGAAC 734
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QY 911 CAAGCTGGTTTATTAATGCTCTCCCGCAGCAGCGGGGCTGGGCCCTGACAGATAT 970
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Db 733 CAAGCTGGTTTATTAATGCTCTCCCGCAGCAGCGGGGCTGGGCCCTGACAGATAT 674
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QY 971 TTCCATTTCTTCTCACTATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCCTG 1030
|||||
Db 673 TTCCATTTCTTCTCACTATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCT-CTG 615
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QY 1031 CGGAGTAGTTGGAAGTTGGAACCGTGTCCAGCACAAGAGGAATCTGTGCAGATGAGCA 1090
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Db 614 CGGAGTAGTTGGAAGTTGGAACCGTGTCCAGCACAAGAGGAATCTGTGCAGATGAGCA 555
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QY 1091 GTCACACTGTTACTCCACAGCGGAGGAGACCTCAGAGAGCCCGAGGATTCGAGGGAAG 1150
|||||
Db 554 GTCACACTGTTACTCCACAGCGGAGGAGACCTCAGAGAGCCCGAGGATTCGAGGGAAG 495
|||||
QY 1151 CAGAGAGTGGAGAACTGGGATTTGAACCCCGCATCTTCCACAGAGCCCATGCTCAA 1210
|||||
Db 494 CAGAGAGTGGAGAACTGGGATTTGAACCCCGCATCTTCCACAGAGCCCATGCTCAA 435
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QY 1211 CCAGTGTGGCGTTCTGCTGCCCTGCGAGTTGGCAGAAAGGATGTTTGTCCCATTTCT 1270
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Db 434 CCAGTGTGGCGTTCTGCTGCCCTGCGAGTTGGCAGAAAGGATG-TTGTGTCCTATTTCT 376
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QY 1271 TGAAGGCCACCGGACAGACCTGACACTAGGTGAGCGGGGGTGC---TGTGGTGGGA 1327
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Db 375 TGAAGGCCACCGGACAGACCTGACACTAGGTGAGCGGGGGTGTGTTGTGGTGGGA 316
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Qy 1388 TGTGTAGTTGAGTCTCTCTGAGACTGCTAAAGTAGGGGAGTGTGTTGCCAGGAC 1447
Db 255 TGTGTAGTTGAGTCTCTCTGAGACTGCTAAAGTAGGGGAGTGTGTTGCCAGGAC 196
Qy 1448 GAATTGAGATAATCTGTCAGTGTGATGAGTGTGATGACACACAGCAGTCTCTAAATC 1507
Db 195 GAATTGAGATAATCTGTCAGTGTGATGAGTGTGATGACACACAGCAGTCTCTAAATC 136
Qy 1508 TTCCTTGTAGGATTATGGTCTCTGCAATCTACAGTTTCTTACTCTTTTGTATCAAAAT 1567
Db 135 TTCCTTGTAGGATTATGGTCTCTGCAATCTACAGTTTCTTACTCTTTTGTATCAAAAT 76
Qy 1568 CACTATCTTCTCATACAGAAATGCCAAGGAGCGGGATCTCGTATCTTTAAAGAGCAG 1627
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Qy 1628 TCCTCTATTCTCAA 1642
Db 15 TCCTCTATTCTCAA 1
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RESULT 4
AL570642/c
LOCUS
DEFINITION
AL570642 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1021Y021 3
prime, mRNA sequence.
ACCESSION
AL570642
VERSION
AL570642.1 GI:12927150
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1031)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
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/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 248 a 297 c 268 g 212 t 6 others
ORIGIN

Query Match 57.2%; Score 973.6; DB 9; Length 1031;
Best Local Similarity 98.2%; Pred. No. 9.8e-156;
Matches 1012; Conservative 3; Mismatches 13; Indels 3; Gaps 3;

Qy 616 GTGGCCACCTGGTGGGGCTCTCAGTCTCTCCAGATGAACCTGGTGGCTGACCTGGTA 675
Db 1031 STGCCCCACCTGGTGGGGCTCTCAGTCTCTCCAGATGAACCTGGTGGCTGACCTGGTA 972

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Qy 676 CAAGAGGTTACAGAGGCCGCCGTGACCTCCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA 735
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Qy 736 TGGAACTCAGACGATCTACCTCCGAAAGCGTCTCTGATGGGCGCGCTGCTTTGGCGTGGTG 795
Db 912 TGGAACTCAGACGATCTACCTCCGAAAGCGTCTCTGATGGGCGCGCTGCTTTGGCGTGGTG 853
Qy 796 ACCACAGGATCTACACAGCGCTGGACTTTTGTCTCTCCAGGAAGGTAGGCCAGCACTGT 855
Db 852 ACCACAGGATCTACACAGCGCTGGACTTTTGTCTCTCCAGGAAGGTAGGCCAGCACTGT 793
Qy 856 GAAGACCCAGCAGGAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 915
Db 792 GAAGACCCAGCAGGAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 733
Qy 916 TGGCTTTTAAATGCTCTCTCCGACAGCGCGGCTTGGGGCCCTGCACAGATATTTCGA 975
Db 732 TGGCTTTTAAATGCTCTCTCCGACAGCGCGGCTTGGGGCCCTGCACAGATATTTCGA 673
Qy 976 TTTCTTCTCCTCATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCTCTGCGGGA 1035
Db 672 TTTCTTCTCCTCATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCTCTGCGGGA 613
Qy 1036 GTAGTTGGAAAGTTGGAACCGTGTCCAGCACACAGAGGAAATCTGTCCAGATGAGCACTAC 1095
Db 612 GTAGTTGGAAAGTTGGAACCGTGTCCAGCACACAGAGGAAATCTGTCCAGATGAGCACTAC 553
Qy 1096 ACTGTTACTCCACAGCGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1155
Db 552 ACTGTTACTCCACAGCGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 493
Qy 1156 AGTGAGGAACTGGGATTTGAACCCGCCATCTTCCAGAGAGCCATGCTCAACCACT 1215
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Qy 1276 GCCACCGGAGACAGCTGACACTAGGCTCAGGCGGGGTGCTGTGGTGGGAGAGGAGCATG 1335
Db 373 GCCACCGGAGACAGCTGACACTAGGCTCAGGCGGGGTGCTGTGGTGGGAGAGGAGCATG 314
Qy 1336 GCTGGGTGGGGTGGGAGAGCTGTTGGCGGTGGTCCAGCTCTTGGCCCTCTGTGTGAG 1395
Db 313 GCTGGGTGGGGTGGGAGAGCTGTTGGCGGTGGTCCAGCTCTTGGCCCTCTGTGTGAG 254
Qy 1396 TTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGTTGCCAGGAGCAATTTGAG 1455
Db 253 TTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGTTGCCAGGAGCAATTTGAG 194
Qy 1456 ATAATATCTGAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1515
Db 193 ATAATATCTGAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 134
Qy 1516 GAGATATGAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
Db 133 GAGATATGAGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 74
Qy 1575 TTTCTGATAACAGAAATGCCAAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1634
Db 73 TTTCTGATAACAGAAATGCCAAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 14
Qy 1635 ATTCTTAAGT 1645
Db 13 TTTCTTGTGT 3

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RESULT 5
AL573044/c
LOCUS
DEFINITION
AL573044 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1014Y005 3

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prime..mRNA sequence.
AL573044
AL573044.1 GI:12931903
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 983
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 230 a 277 c 252 g 219 t 5 others
ORIGIN

Query Match 56.1%; Score 953.8; DB 9; Length 983;
Best Local Similarity 99.0%; Pred. No. 2.3e-152;
Matches 975; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

QY 665 CTGACCTGGTACAGAGTTTCAGAGGCCCTGACCTCCAGACAGAGGTGGGCCCATGT 724
DB 983 CTGACCTGGTACAGAGTTTCAGAGGCCCTGACCTCCAGACAGAGGTGGGCCCATGT 924
QY 725 CCCGATGTCATGGAATCAGACGATCTACTCCGAGCGCTCTGATGGCCCTGCTT 784
DB 923 CCCGATGTCATGGAATCAGACGATCTACTCCGAGCGCTCTGATGGCCCTGCTT 864
QY 785 TGGCTGGTGACACAGGCAATCTACAGCGCTGGACTTTGGTTCTCTCCAGGAAGGTAG 844
DB 863 TGGCTGGTGACACAGGCAATCTACAGCGCTGGACTTTGGTTCTCTCCAGGAAGGTAG 804
QY 845 CCCAGCACTGTGAAGACCCAGCAGAGCCAGCTGAGTGAGCCACAGACCACTGCTTC 904
DB 803 CCCAGCACTGTGAAGACCCAGCAGAGCCAGCTGAGTGAGCCACAGACCACTGCTTC 744
QY 905 TGAACCTCAAGCTGCTTTATTATATGCTCTCCGACACAGCCGGCTTGGGCCCTGCAC 964
DB 743 TGAACCTCAAGCTGCTTTATTATATGCTCTCCGACACAGCCGGCTTGGGCCCTGCAC 684
QY 965 AGATATTTCATTTCTCCACATNTGACACTGAGCAAGATCTTGCTCCACTAAATGAG 1024
DB 683 AGATATTTCATTTCTCCACATNTGACACTGAGCAAGATCTTGCTCCACTAAATGAG 624
QY 1025 CTCTCGGGGAGTAGTTGGAACCTGGTCCAGCAGAGAGGATCTGTGCACA 1084
DB 623 CT-CTCGGGGAGTAGTTGGAACCTGGTCCAGCAGAGAGGATCTGTGCACA 565
QY 1085 TGAGCAGTACACTGTACTCCACAGCGGAGGAGACCACTCAGAGGCCCGAGGAATCGGA 1144
DB 564 TGAGCAGTACACTGTACTCCACAGCGGAGGAGACCACTCAGAGGCCCGAGGAATCGGA 505

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QY 1145 GCGAAGCAGAGAGGTGGAGAACTGGGATTGTAACCCCGCCCATCTTCCACAGAGCCCAT 1204
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QY 1205 GCTCAACCACTGTGGCGTTCTGCTGCCCTCGAGTTGGCAAGAGGATGTTTTGTGCCA 1264
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QY 1325 GGAGAGCATGGTGGGTGGGGTGGGAGACCTGCTGGCGGTGGTGGCGCTTTGGC 1384
DB 325 GGAGAGCATGGTGGGTGGGGTGGGAGACCTGCTGGCGGTGGTGGCGCTTTGGC 266
QY 1385 CCCGTGTGAGTTGAGTCTCTCTGAGACTGCTAGTAGTAGGGGCGAGTGATGTTGCCAG 1444
DB 265 CCCGTGTGAGTTGAGTCTCTCTGAGACTGCTAGTAGTAGGGGCGAGTGATGTTGCCAG 206
QY 1445 GACGAATTGAGATAATATCTGTGAGTGTGATGATGATGATGATGATGATGATGATGAT 1504
DB 205 GACGAATTGAGATAATATCTGTGAGTGTGATGATGATGATGATGATGATGATGATGAT 146
QY 1505 ATCTTCCTCTGAGGATATGGTCTGCAATCTACAGTTCTTACTGTTTGTATCAA 1564
DB 145 ATCTTCCTCTGAGGATATGGTCTGCAATCTACAGTTCTTACTGTTTGTATCAA 86
QY 1565 AATCACTATCTTCTGATACAGAAATGCCAGGCGAGGATCTCGTATCTTTAAAG 1624
DB 85 AATCACTATCTTCTGATACAGAAATGCCAGGCGAGGATCTCGTATCTTTAAAG 26
QY 1625 CACTCTCTTATTCCTAAGGTAATC 1649
DB 25 CACTCTCTTATTCCTAAGGTAATC 1

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RESULT 6
LOCUS AL548504
DEFINITION AL548504 LTI_NFL006_PL2 Homo sapiens cDNA clone EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL548504
VERSION AL548504.1 GI:12883573
KEYWORDS EST.
SOURCE human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 956
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/tissue_type="placenta"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL :

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BASE COUNT	194 a	288 c	318 g	155 t	1 others
ORIGIN	http://fulllength.invitrogen.com"				

Query Match 54.9%; Score 933.2; DB 9; Length 956;
Best Local Similarity 99.6%; pred. No. 7.1e-149;
Matches 946; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

[illegible]

RESULT 7
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DEFINITION	AL522777.1 LTI_NFL003_NBC3 primo, mRNA sequence.	Homo sapiens	cDNA clone	CS0DC026P18.5
ACCESSION	AL522777.1			
VERSION	AL522777.1	GI:12791264		
KEYWORDS	Est.			
SOURCE	human.			

SOURCE
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 973)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..973

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Reng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : rliang@lifetech.com URL :
http://fulllength.invitrogen.com"
195 a 290 c 319 g 166 t 3 others

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BASE COUNT
ORIGIN

Query Match	54.3%	Score 924;	DB 9;	Length 973;
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135	AGACCCGCCCATGACGCCGTTCTCGTGGTCTGCTGCATCTCGGTGTGCTGCAGCGTGTGAG	194		
121	AGACCCGCCCATGACGCCGTTCTCGTGGTCTGCTGCATCTCGGTGTGCTGCAGCGTGTGAG	180		
195	CAGCGAGGTGACCGAGGTCAGTTCCTATGCTCGGGGCGCTGGTCAAGCGCAAGCTGG	253		
181	CAGCGAGGTGACCGAGGTCAGTTCCTATGCTCGGGGCGCTGGTCAAGCGCAAGCTGGN	240		
254	AGCCGCTGCAGAGGGGCGCTAGACCTCTTCTCATGCTGTGGAGCAGACGACCTGGAGC	313		
241	AGCCGCTGCAGAGGGGCGCTAGACCTCTTCTCATGCTGTGGAGCAGACGACCTGGAGC	300		
314	CCGGGCACACCGAGCTCCTGCGCGAGCTGCTGCCTCCCTCGGCGCCACGACCTGCTGC	373		
301	CCGGGCACACCGAGCTCCTGCGCGAGCTGCTGCCTCCCTCGGCGCCACGACCTGCTGC	360		
374	GGCGCTCGAGGACTTCGAGGCGGGGCGCGCGCGCGCGCGCTGGGGAGAGAGACC	433		


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QY 859 GACCAGCAGGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 918
DB 841 GACCAGCAGGAGCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 900
QY 919 GTTATTATGTC 930
DB 901 GTTATTATGTC 912

RESULT 9
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LOCUS AL562839 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC019YA19 3
DEFINITION prime, mRNA sequence.
ACCESSION AL562839
VERSION AL562839.1 GI:12911659
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC019YA19"
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 226 a 273 c 244 g 198 t 14 others
ORIGIN

Query Match 51.3%; Score 872.8; DB 9; Length 955;
Best Local Similarity 96.4%; Pred. No. 1.3e-138;
Matches 922; Conservative 10; Mismatches 18; Indels 6; Gaps 4;

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QY 750 ATCTACCTCCGAGGCTGATGGCGCGTGTTCGCTGGTGGACACAGGATCTA 809
DB 835 ATCTACCTCCGAGGCTGATGGCGCGTGTTCGCTGGTGGACACAGGATCTA 776
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QY 870 AACCCAGGCTGAGTGAGCCACAGACCACTGCTTCTGAAGTCAAGCTGC 929
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QY 930 CTTCTCCCGCACCAGCGGGCTTGGGCCCTGCACAGATATTTCCATTTCTTCCCTACTA 989
DB 655 CTTCTCCCGCACCAGCGGGCTTGGGCCCTGCACAGATATTTCCATTTCTTCCCTACTA 596
QY 990 TGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCTCTCGGGAGTAGTTGGAAGTT 1049
DB 595 TGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCTCTCGGGAGTAGTTGGAAGTT 536
QY 1050 GGAACCGTGTCCAGCACAGAGGAATCTGTGCAGATCAGCAGTCACTGTTACTCCACA 1109
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QY 1110 GCGGAGGAGACCACTCAGAGGCCCGAGGATCGAGGAGGAGAGAGGTGGAGAACTGG 1169
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QY 1170 GATTGAACCCCGCCCATCTTCCAGAGAGCCCATCTCAACACACTGTGGCGTCTCTGCTG 1229
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DB 355 CCCCTGCAGTTGGCAGAAAGGATG-TTATGTCCATTTCTTGGAGGCCACCGGACAGAGA 297
QY 1290 CTTGGACACTAGGCTCAGCGGGGTGC---TGTGTGGGAGAGAGCATGGCTGGGGTGGG 1346
DB 296 CTTGGACACTAGGCTCAGCGGGGTGC-TTATGTCCATTTCTTGGAGGCCACCGGACAGAGA 237
QY 1347 GGTGGGAGACCTGTTGGCGCTGTCAGCTCTTGGCCCTGTGTGAGTTGAGTCTCTCT 1406
DB 236 GGTGGGAGACCTGTTGGCGCTGTCAGCTCTTGGCCCTGTGTGAGTTGAGTCTCTCT 177
QY 1407 CTTGAGACTGCTAAGTAGGGGAGTGTGTCAGGAGCAATGAGATAATATCTGT 1466
DB 176 CTTGAGACTGCTAAGTAGGGGAGTGTGTCAGGAGCAATGAGATAATATCTGT 117
QY 1467 GAGGTGCTGATGAGTGATGACACACACACTCTCTAAATCTTCCCTTGTGAGGATATGG 1526
DB 116 GAGGTGCTGATGAGTGATGACACACACACTCTCTAAATCTTCCCTTGTGAGGATATGG 57
QY 1527 GTCCTGCAATTTCTACAGTTCTTACTGTTTGTATCAAAATCACTATCTTCTGTAT 1582
DB 56 CTCCTGCAATTTCTACAGTTCTTACTGTTTGTATCAAAATCACTATCTTCTGTAT 1

RESULT 10
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LOCUS AL521788 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB003YK15 3
DEFINITION prime, mRNA sequence.
ACCESSION AL521788
VERSION AL521788.1 GI:12785281
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 961)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 961
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/db_xref="taxon:9606"

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FEATURES
source


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DEFINITION AL518571 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA09Y01 5
prime, mRNA sequence.
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VERSION AL518571.1 GI:12782064
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/tissue_type="neuroblastoma cells"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen, 9800 Medical Center Drive, Rockville
Maryland 20850, USA Fax : (1) 301 610 8371 Email :
filang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 189 a 273 c 311 g 154 t 5 others
ORIGIN

Query Match 48.6%; Score 827; DB 9; Length 932;
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QY 840 GGTAGCCCGACAGCTGTGAAGACCCAGGAGCGGCTGAGTGGAGCCACAGACCACT 899
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ACCESSION AL556073
VERSION AL556073.1 GI:12898410
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 BASE COUNT 175 a 253 c 288 g 133 t 10 others
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 prime, mRNA sequence.
 ACCESSION AL517525
 VERSION AL517525.1 GI:12781018
 KEYWORDS EST
 SOURCE human.
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 REFERENCE 1 (bases 1 to 859)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
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 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 Bp 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 BASE COUNT 208 a 240 c 218 g 188 t 5 others
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Sun Aug 18 12:47:10 2002

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QY	1326	GAGAGCATGGCTGGGGTGGGGTGGGAGAGCTGTTGGCCGTGGTCCAGCTCTTGGCC	1385
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QY	1386	CCTGTGTGAGTTGAGTCTCCTCTCTCAGACTGCTAAGTAGGGGCGAGTGTTGCCAGG	1445
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Search completed: August 17, 2002, 01:10:14
Job time: 1979 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2002, 00:25:50 ; Search time 60.78 seconds
(without alignments)
467.833 Million cell updates/sec

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Perfect score: 1302
Sequence: 1 VNOAPCRFGGILGLPLGRK.....RSGNMPMSWNSDASTSEAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1299	99.8	256	AAW11894	MORT-1 modulator
3	1047	80.4	208	AAW11894	Human FADD protein
4	1040	79.9	208	AAW11894	FADD (Fas-associat
5	1040	79.9	208	AAW11894	Human FADD protein
6	1040	79.9	208	AAW11894	Human FADD prodona
7	1033	79.3	208	AAW11894	Human FADD. Homo
8	1028	79.0	208	AAW11894	Amino acid sequenc
9	983.5	75.7	201	AAW87492	Amino acid sequenc
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11	719.5	55.3	205	AAW11894	Mouse apoptosis me

12	401	30.8	83	22	AAW84800	FADD death effecto
13	401	30.8	83	22	AAW61115	Human FADD DED1 do
14	375	28.8	81	19	AAW76623	Human FADD protein
15	370.5	28.5	117	22	AAW61902	Mouse apoptosis me
16	349	26.8	88	22	AAW61901	Mouse apoptosis me
17	318	24.4	62	17	AAW00210	Human MORT-1 prote
18	125.5	9.6	480	22	AAE06523	Mouse caspase 8 pr
19	122.5	9.4	239	22	ABW62302	Drosophila melanog
20	122	9.4	180	22	AAW84803	Human caspase 8 pr
21	122	9.4	180	22	AAW61118	Human Caspase-8.
22	122	9.4	220	19	AAW75961	MORT-1 binding pro
23	122	9.4	235	18	AAW11892	Cell death-associat
24	122	9.4	261	18	AAW31735	MACH isoform beta4
25	122	9.4	277	18	AAW11893	MACH isoform beta3
26	122	9.4	464	18	AAW11895	MACH isoform alpha
27	122	9.4	479	18	AAW31523	Interleukin-1 beta
28	122	9.4	479	18	AAW11891	MACH isoform alpha
29	122	9.4	479	19	AAW75963	Human Caspase-8.
30	122	9.4	479	22	AAE00605	Human caspase 8 L7
31	122	9.4	479	22	AAW84812	Human caspase 8 L7
32	117	9.0	479	22	AAW84813	Human caspase 8 mu
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37	116.5	8.9	81	19	AAW75962	Human Caspase-81.
38	116	8.9	83	22	AAW84796	Caspase 8 death ef
39	116	8.9	83	22	AAW61111	Human caspase-8 DE
40	116	8.9	110	22	ABW30659	Peptide #3310 enco
41	116	8.9	110	22	ABW35830	Peptide #3336 enco
42	116	8.9	110	22	ABW21245	Protein #3244 enco
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ALIGNMENTS

RESULT 1
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ID AAW11894 standard; Protein; 256 AA.
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AC AAW11894;
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DT 29-OCT-1997 (first entry)
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DE Modulator of cellular toxicity (MORT-1).
XX
KW MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death;
KW antibody; Fas ligand receptor; Fas-R; death domain region; septic shock;
KW tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death;
KW apoptosis/programmed cell death; p53-R; graft rejection; acute hepatitis;
KW autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
TNF; therapy.
XX
OS Homo sapiens.
XX
PN WO9703998-A1.
XX
PD 06-FEB-1997.
XX
PF 14-JUN-1996; 96WO-US10521.
XX
PR 16-APR-1996; 96IL-0117932.
PR 16-JUL-1995; 95IL-0114615.
PR 17-AUG-1995; 95IL-0114986.
PR 14-SEP-1995; 95IL-0115319.
PR 27-SEP-1995; 95IL-0115586.
XX
PA (WEIN/) WEINWURZEL H.
XX (YEDA) YEDA RES & DEV CO LTD.

PI Boldin M, Goltsev YV, Goncharov T, Wallach D;
 XX WPI; 1997-132570/12.
 DR N-PSDB; AAT61397.

XX New DNA encoding MACH protein that interacts with MORT-1 protein -
 PT to mediate intracellular effects of FAS or TNF receptors, partic.
 PT for regulating apoptosis in tumours, virus-infected cells etc.
 XX

PS Disclosure; Page 102-103; 163pp; English.

XX This sequence represents the mediator of cellular toxicity (MORT-1)
 CC protein. This sequence is bound by the protein of the invention (see
 CC AAW1892), designated MACH. MORT-1 binds to the FAS ligand receptor
 CC (FAS-R) death domain region, and triggers part of the cell death
 CC signalling cascade in mammalian cells. Vectors containing MACH, the MACH
 CC protein, and antibodies (Ab) against it are used to modulate the effect
 CC of FAS-R ligand or TNF on cells that carry FAS-R or p55-R. This is
 CC specifically for treating tumours, HIV-infected cells or other diseased
 CC cells, by control of apoptosis/programmed cell death. The MACH protein is
 CC a mediator of the cell death pathway initiated by TNF and FAS-R binding,
 CC i.e. it mimics or enhances the effect of MORT-1 where increased
 CC cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases
 CC of septic shock, graft rejection and acute hepatitis, sequences encoding
 CC antisense molecules or ribozymes, or Ab against MACH, are used.
 CC Compounds that inhibit MACH are potentially useful for controlling MACH
 CC activity e.g. in cases of autoimmune disease, oligodendrocyte death in
 CC multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can
 CC also be used to isolate and characterise other proteins and receptors
 CC involved in signalling and for Ab production. The Ab can be used to
 CC purify the new proteins and for diagnosis of conditions involving
 CC abnormal function of FAS-R mediated cellular effects.

XX Sequence 256 AA;

Query Match 100.0%; Score 1302; DB 18; Length 256;
 Best Local Similarity 100.0%; Pred. No. 2.3e-125;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 sllssseltekflclgrvvkrklervqsgldfslmleqndlepghltellreillaslr 120
 QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDWRRRLAROLKVSdTIDSTEDR 180
 DB 121 hdlrrvddfeagaaagapgeedlcaafnvicdnygkdwrrrlarolkvsdtkidsiedr 180
 QY 181 YPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLADLVQEVQOARDLQNRSGA 240
 DB 181 yprnltervreslrwktekenatvahlvglalrsqmnvladvlqvqvgardlqnrsga 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 mspmswnsdastseas 256

RESULT 2

AA98346
 ID AAR98346 standard; Protein; 256 AA.

AC AAR98346;

XX 13-SEP-1996 (first entry)

DE MORT-1 modulator of FAS receptor.

XX MORT-1; HFI; FAS/APOL receptor; FAS-R; tumour; cancer; HIV;
 KW mediator of receptor toxicity; gene therapy.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 160..221
 FT /label= Death domain
 FT
 XX WO9618641-A1.
 PN
 XX 20-JUN-1996.
 PD
 XX 14-DEC-1995; 95WO-US16542.
 PF
 XX 16-JUL-1995; 95IL-0114615.
 PR
 XX 15-DEC-1994; 94IL-0112022.
 PR
 XX 19-FEB-1995; 95IL-0112692.
 XX
 XX (WEIN/) WEINWURZEL H.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA

XX Boldin M, Mett I, Varfolomeev E, Wallach D;

XX WPI; 1996-300569/30.

XX N-PSDB; AAT30372.

XX MORT-1 protein capable of interacting with FAS-R intracellular
 PT domain - useful for modulating FAS-R ligand effect on cells and
 PT treating, e.g. tumour cells and HIV-infected cells
 PT

XX Claim 5; Fig 4; 72pp; English.

XX MORT-1 (AAR98346) (Mediator of Receptor Toxicity), also designated HFI,
 CC is a novel protein that binds to the intracellular domain (FAS-IC) of
 CC the FAS ligand receptor FAS-R (or FAS/APOL), and is capable of
 CC modulating the function of FAS-R. MORT-1 is also capable of
 CC self-association and can activate cell cytotoxicity on its own.
 CC Recombinant MORT-1 can be obtd. from host cells transformed with a
 CC vector carrying a cDNA clone (AAT30372) isolated from HeLa cells.
 CC MORT-1 can be used to modulate the FAS-R ligand on cells carrying
 CC an FAS-R. It can also be used to treat tumour cells or HIV-infected
 CC cells, or to raise antibodies.

XX Sequence 256 AA;

Query Match 99.8%; Score 1299; DB 17; Length 256;
 Best Local Similarity 99.6%; Pred. No. 4.7e-125;
 Matches 255; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNOAPECRFGGILGPKGRDLARASEPTREGARRAGPOPRPLADPAMPDFVLVLSHS 60
 DB 1 vnoapecrfggildgpkgrdlaraseptregarragpprpladpampdfvlvlhs 60
 QY 61 SLSLSSELTKFLCLGRVVKRKLERSVQGLDLFSLLEQNDLEPGHTELLRELLASLR 120
 DB 61 sllssseltekflclgrvvkrklervqsgldfslmleqndlepghltellreillaslr 120
 QY 121 HDLLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNYGKDWRRRLAROLKVSdTIDSTEDR 180
 DB 121 hdlrrvddfeagaaagapgeedlcaafnvicdnygkdwrrrlarolkvsdtkidsiedr 180
 QY 181 YPRNLTERVRESLRWKTEKENATVAHLVGLALRSQMNVLADLVQEVQOARDLQNRSGA 240
 DB 181 yprnltervreslrwktekenatvahlvglalrsqmnvladvlqvqvgardlqnrsga 240
 QY 241 MSPMSWNSDASTSEAS 256
 DB 241 mspmswnsdastseas 256

RESULT 3

AA51329
 ID AAV51329 standard; Protein; 208 AA.

```

XX AC AAY51329;
XX DT 19-APR-2000 (first entry)
XX DE Human FADD protein.
XX KW FADD; human; antisense; inhibitor; Fas-associated death domain.
XX OS Homo sapiens.
XX PN US6015712-A.
XX PD 18-JAN-2000.
XX PF 19-JUL-1999; 99US-0357072.
XX PR 19-JUL-1999; 99US-0357072.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Cowsett LM, Baker BF, Zhang H;
XX WPI; 2000-126316/11.
XX DR N-PSDB; AAZ44745.
XX PT Antisense oligonucleotides, useful for inhibiting human Fas-associated
XX death domain (FADD) expression are targeted to the 3' untranslated
XX region of the FADD gene -
XX Example 13; Column 43-46; 37pp; English.
XX This invention describes novel antisense oligonucleotides (OGNs) (I)
XX 8-20 nucleotides in length that specifically hybridize with and inhibit
XX nucleic acids encoding human Fas-associated death domain (FADD),
XX targeted to the 3' untranslated region (3'UTR). (I) can be used to treat
XX animals, especially humans, suspected of having or being prone to a
XX disease or condition associated with FADD expression. This sequence
XX represents the human FADD protein described in the method of the
XX invention.
XX Sequence 208 AA;
XX
Query Match 80.4%; Score 1047; DB 21; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.8e-99;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 MDPTLVLLHVSSSLSSSELTCLKFLCLGRVVRKKLERVQSLDLFSMLLEQNLDLEPGHT 108
DB 1 mdptlvllhvssslssseitclkflclgrvvrkklerqvsgldlfsmlleqndlepght 60
QY 109 ELRLRELLASLRHDLRRVDDFAGAAAGAAPGEEDLCRAFNVICDNVGVKDWRLARQLK 168
DB 61 ellrrellaslrhdlrrvddfagaaagapgeedlcaafnvicdnvkvdkwrlarqlk 120
QY 169 VSDTKIDISIEDPRNTERVRESLRIRKNTKENATVAHLVGLRSCQMNVLVADLVQEV 228
DB 121 vsdtkidsiedprnltervreslriwntekenatvahlvgalscqmnlvadvlvqev 180
QY 229 QQARDLQNRSGAMPKSNWSDASTSEAS 256
DB 181 qqardlqnrsgampkswnsdastseas 208
RESULT 4
ID AA003653
XX AA003653 standard; Protein; 208 AA.
XX AC AA003653;
XX DT 22-FEB-1997 (first entry)
XX

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```

DE XX FADD (Fas-associating protein with novel death domain) protein.
KW XX Human; FADD; Fas-associating protein with novel death domain;
KW XX apoptosis; Fas receptor; death domain; gene therapy; antibody;
KW XX immunoassay; drug screening; diagnostic; AIDS; antiinflammatory;
KW XX antitumour; cerebroprotective; neuroprotective.
OS XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..125
XX FT /note= "N-terminal fragment, inducing apoptosis but
XX FT /note= not binding to Fas receptor"
XX FT Region 35..208
XX FT /note= "C-terminal active fragment"
XX FT Region 41..208
XX FT /note= "C-terminal active fragment"
XX FT Region 42..208
XX FT /note= "Fas receptor-binding NFD-2 polypeptide"
XX FT Region 61..208
XX FT /note= "Fas receptor-binding NFD-3 polypeptide"
XX FT Region 80..208
XX FT /note= "Fas receptor-binding NFD-4 polypeptide"
XX FT Misc-difference 121
XX FT /note= "Altered to Asn in FADDmt mutant"
XX FT Domain 111..177
XX FT /note= "Death domain"
XX PN W09631603-A2.
XX
XX 10-OCT-1996.
XX
XX 28-FEB-1996; 96WO-US02857.
XX
XX 18-MAY-1995; 95US-0443982.
XX 03-APR-1995; 95US-0416379.
XX (UNMI ) UNIV MICHIGAN.
XX
XX Dixit VM, O'Rourke K;
XX WPI; 1996-465026/46.
XX N-PSDB; AAT39397.
XX
XX FADD protein that binds to cytoplasmic region of Fas receptor - for
XX identifying inhibitors of Fas-associated apoptosis useful for
XX treating e.g. AIDS, leukaemia, stroke, etc
XX Example 1; Fig 2A-B; 96pp; English.
XX
XX The sequence corresponds to FADD (Fas-associating protein with novel
XX death domain), which binds the cytoplasmic region of a Fas receptor,
XX and modulates apoptosis induced by activation of the receptor by
XX ligand binding. The FADD cDNA has been isolated using a yeast
XX two-hybrid system to screen for proteins interacting with the Fas
XX cytoplasmic domain. The protein contains a death domain, with
XX interacts with the death domain of Fas. Mutation of Val-121 to
XX Asn in mutant FADDmt disrupts binding and/or signalling properties.
XX C-terminal polypeptides NFD-2, NFD-3 and NFD-4 bind the Fas receptor
XX cytoplasmic domain in vitro. An N-terminal fragment induces
XX apoptosis but does not bind the Fas receptor. The encoding DNA may
XX be used in gene therapy, and the protein or a corresponding antibody
XX may be used to screen for agents modulating FADD pathway cellular
XX functions and Fas-associated apoptosis, for use in therapy of e.g.
XX AIDS, inflammation, leukaemia, myocardial infarction, degenerative
XX disease, etc.
XX
XX Sequence 208 AA;
XX

```

Query Match 79.9%; Score 1040; DB 17; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLLHSVSSLSSELTELKFLCGRVVKRKLERSVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdplvllhsvsslsseletelkflcgrvgrklierqsgldlfsmlleqndlepght 60
 QY 109 ELIRELLASLRHDLRRVDDFAGAAAGAPGEEDLCAAFNVICDNVGVKDWRRRLARQLK 168
 DB 61 ellirellaslrhdlrrvddfeagaaagaapeedlcaafnvicdnvkvdkwrrlarqlk 120
 QY 169 VSDTKIDSIEDRYPRNLTERVRESRLRWKTEKENATVAHLVGLRSCQNMNLVADLVQEV 228
 DB 121 vsdtkidsiedryprnltervresrlrwnktenatvahlvgalrscqnmnlvadvlqv 180
 QY 229 QQARDLQNRSGAMSPMWSNDASTSEAS 256
 DB 181 qqardlqnrsgamspmwnsdastseas 208
 RESULT 5
 AAW96154
 ID AAW96154 standard; Protein; 208 AA.
 AC AAW96154;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE Human FADD protein.
 KW FIP; FADD interacting protein; FADD; Fas-associated protein with a
 KW novel death domain; cell death; apoptosis; Alzheimer's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; muscular dystrophy;
 KW amyotrophic lateral sclerosis; virus; bacteria; fungus; mycoplasma;
 KW protozoa; neoplasia; dysplasia; hyperplasia.
 XX
 OS Homo sapiens.
 XX
 PN WO9900499-A1.
 XX
 PD 07-JAN-1999.
 XX
 PF 26-JUN-1998; 98WO-US13320.
 XX
 PR 03-JUN-1998; 98US-0087886.
 PR 26-JUN-1997; 97US-0050792.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chen TT, Williams LT;
 XX
 XX WPI; 1999-095745/08.
 DR N-PSDB; AAX08910.
 XX
 XX New FADD (Fas-associated protein with a novel death
 PT domain)-interacting protein - useful for inducing or preventing
 PT apoptosis in a cell, to aid in controlling apoptosis-related
 PT diseases
 XX
 PS Disclosure; Page 47; 58pp; English.
 XX
 CC An epitope of human FADD (Fas-associated protein with a novel
 CC death domain)-interacting protein (FIP protein) comprising amino
 CC acids 348-727 of the protein described in AAW96153, can be used to
 CC induce or prevent apoptosis in a cell. Specifically, decreasing the
 CC levels of FIP348-727 prevents apoptosis. This is useful in cells
 CC which are dying prematurely, eg: Alzheimer's disease, Acquired
 CC Immune Deficiency Syndrome (AIDS), muscular dystrophy, amyotrophic
 CC lateral sclerosis (and other muscle wasting diseases), autoimmune
 CC diseases, and diseases where cells are infected with a pathogen
 CC (virus, bacteria, fungus, mycoplasma or protozoa). Increasing the
 CC levels of FIP 348-727 induces apoptosis which is useful in cells
 CC suffering from neoplasias, dysplasias, hyperplasias, or their
 CC symptoms. Purified and isolated FIP subgenomic polynucleotides are
 CC useful as primers to obtain more copies of the nucleotides, and as

CC probes that identify wild-type or mutant coding sequences. They are
 CC also useful for expressing FIP mRNA, proteins or fusion proteins,
 CC and in the generation of FIP antisense oligonucleotides and
 CC ribozymes. They are also useful in expression constructs and in
 CC gene delivery vehicles (optionally in combination with a condensing
 CC agent) that deliver FIP mRNA or oligonucleotides, FIP proteins
 CC (including variants), FIP-specific ribozymes or single-chain
 CC antibodies into eukaryotic cells. This is the human FADD protein.
 CC Human FIP protein binds to amino acids 1-110 of this sequence.
 XX
 SQ Sequence 208 AA;
 Query Match 79.9%; Score 1040; DB 20; Length 208;
 Best Local Similarity 99.5%; Pred. NO. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 49 MDPLVLLHSVSSLSSELTELKFLCGRVVKRKLERSVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdplvllhsvsslsseletelkflcgrvgrklierqsgldlfsmlleqndlepght 60
 QY 109 ELIRELLASLRHDLRRVDDFAGAAAGAPGEEDLCAAFNVICDNVGVKDWRRRLARQLK 168
 DB 61 ellirellaslrhdlrrvddfeagaaagaapeedlcaafnvicdnvkvdkwrrlarqlk 120
 QY 169 VSDTKIDSIEDRYPRNLTERVRESRLRWKTEKENATVAHLVGLRSCQNMNLVADLVQEV 228
 DB 121 vsdtkidsiedryprnltervresrlrwnktenatvahlvgalrscqnmnlvadvlqv 180
 QY 229 QQARDLQNRSGAMSPMWSNDASTSEAS 256
 DB 181 qqardlqnrsgamspmwnsdastseas 208
 RESULT 6
 AAB84804
 ID AAB84804 standard; Protein; 208 AA.
 XX
 AC AAB84804;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE Human FADD prodomain.
 XX
 KW NF-kappaB; JNK; apoptosis; death effector domain; DED.
 XX
 OS Homo sapiens.
 XX
 PN US6207458-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 07-MAY-1998; 98US-0074044.
 XX
 PR 07-MAY-1998; 98US-0074044.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Chaudhary PM, Hood L;
 XX
 XX WPI; 2001-342087/36.
 XX
 PT Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteinaceous species having two death effector domain and test
 PT compound
 XX
 PS Disclosure; Column 51-52; 62pp; English.
 XX
 CC The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic

CC applications and are useful for regulating cellular NF-kappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.
 CC The present sequence is a prodomain used in the invention.
 XX
 SQ Sequence 208 AA;

Query Match 79.9%; Score 1040; DB 22; Length 208;
 Best Local Similarity 99.5%; Pred. No. 1.4e-98;
 Matches 207; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 Db 1 mdpflvllhsvsslsesselteklfcgrvgrkrlervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDNGKDWRRRLARQLK 168
 Db 61 ellrellaslrhdlrrvddfeagaaagaeedlcaafnvicdngkdwrrrlarqlk 120
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWNTKENATVAHLVGLRSCQMNVLVADLVQEV 228
 Db 121 vsdtkidsiedryprnltervreslrwntekenatvahlvglrscqmnvlvadvlqev 180
 QY 229 QQARDLQNRSGAMSPMNSDASTSEAS 256
 Db 181 qqardlqnrsgamspmswnsdastseas 208

RESULT 7
 AAB61119
 ID AAB61119 standard; protein; 208 AA.
 AC AAB61119;
 DT 02-MAY-2001 (first entry)
 DE Human FADD.
 XX
 XX Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
 KW Jun N-terminal kinase; JunK; apoptosis; Caspase-8 mutant.
 XX
 OS Homo sapiens.
 XX
 PN US6160095-A.
 XX
 PD 12-DEC-2000.
 XX
 PF 24-AUG-1999; 98US-0382155.
 XX
 PR 07-MAY-1998; 98US-0074044.
 PA (UNIW) UNIV WASHINGTON.
 PA (STOW-) STOWERS INST MEDICAL RES.
 XX
 PI Hood L, Chaudhary PM;
 XX
 DR WPI; 2001-101569/11.
 XX
 PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
 PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
 PT for therapeutic purposes -
 XX
 PS Example 8; Fig 11; 60pp; English.
 XX
 CC The present sequence has been shown to regulate the nuclear factor-kappa
 CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
 CC is provided in a specification relating to novel mutants (D73A, L74A and
 CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
 CC and apoptosis activities. The Caspase-8 mutants are useful for
 CC therapeutic purposes and in test methods or assays for determining
 CC whether a candidate compound has a significant effect upon cell

CC activities, especially NF-kB, JunK and apoptosis, so as to facilitate the
 CC discovery and/or design of therapeutic agents.
 XX
 SQ Sequence 208 AA;

Query Match 79.3%; Score 1033; DB 22; Length 208;
 Best Local Similarity 99.0%; Pred. No. 7.5e-98;
 Matches 206; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 MDPFLVLLHSVSSLSSELTELKFLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 Db 1 mdpflvllhsvsslsesselteklfcgrvgrkrlervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDNGKDWRRRLARQLK 168
 Db 61 ellrellaslrhdlrrvddfeagaaagaeedlcaafnvicdngkdwrrrlarqlk 120
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWNTKENATVAHLVGLRSCQMNVLVADLVQEV 228
 Db 121 vsdtkidsiedryprnltervreslrwntekenatvahlvglrscqmnvlvadvlqev 180
 QY 229 QQARDLQNRSGAMSPMNSDASTSEAS 256
 Db 181 qqardlqnrsgamspmswnsdastseas 208

RESULT 8
 AAW87493
 ID AAW87493 standard; Protein; 208 AA.
 AC AAW87493;
 DT 12-FEB-1999 (first entry)
 DE Amino acid sequence of MORT1 Isoform MORT1G173A from human brain.
 KW MORT1; MORT1del21; NTERA2; CNS; Isoform; death domain; Fas/APOL;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9849297-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 14-APR-1998; 98WO-US07439.
 XX
 PR 25-APR-1997; 97US-0044835.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Bingham BW, Birsan C, Wood AT, Young KH;
 XX
 DR WPI; 1999-009424/01.
 DR N-PSDB; AAV71930.
 XX
 PT Human, neuronal MORT1 isoform(s) - used as screening agents in
 PT diagnosing CNS diseases, and in discovering CNS-specific
 PT anti-apoptotic compounds
 XX
 PS Claim 7; Pages 30-31; 31pp; English.
 XX
 CC This represents the amino acid sequence of a MORT1 isoform MORT1G173A.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209019. The cDNA has a nucleotide substitution (G
 CC to A) at basepair position 173 of the published MORT1 coding sequence.
 CC The invention relates to three MORT1 nucleic acid isoforms (AAV71928 to
 CC AAV71930) that encode proteins which can interact with the death domain
 CC of Fas/APOL. The MORT1 isoforms can also interact with MACH alpha1 or
 CC other members of the ICE/Ced3 (caspase) family of proteins. The
 CC transcript isoforms, together with their encoded proteins are useful as

CC screening agents in diagnosing CNS diseases, and in discovering
 CC CNS-specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.
 XX SQ Sequence 208 AA;
 Query Match 79.0%; Score 1028; DB 20; Length 208;
 Best Local Similarity 98.6%; Pred. No. 2.5e-97;
 Matches 205; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 49 MDPFLVLLHSVSSSSSELTEKLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslseseltelkclgrvgrkrlervqsgdlfsmleqndlepeht 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 168
 DB 61 ellrellaslrhdlrrvddfeagaaagapgeedlcaafnvicdnvkgdkwrrlarqlk 120
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
 DB 121 vadtksiedryprnltervreslrwktekenatvahlvglrscqmnlaadlvgev 180
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 181 qqardlqnrsgamspmswnsdastseas 208
 RESULT 9
 AAW87492
 ID AAW87492 standard; Protein; 201 AA.
 XX AC AAW87492;
 XX DT 12-FEB-1999 (first entry)
 XX DE Amino acid sequence of MORT1 isoform MORT1del21 from human brain.
 KW MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/AP01;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 XX OS Homo sapiens.
 XX PN WO9849297-A1.
 XX PD 05-NOV-1998.
 XX PF 14-APR-1998; 98WO-US07439.
 XX PR 25-APR-1997; 97US-0044835.
 XX PA (AMHP) AMERICAN HOME PROD CORP.
 XX PI Bingham BW, Birsan C, Wood AT, Young KH;
 XX DR WPI; 1999-009424/01.
 XX DR N-PSDB; AAV71929.
 XX PT Human, neuronal MORT1 isoform(s) - used as screening agents in
 XX PT diagnosing CNS diseases, and in discovering CNS-specific
 XX PT anti-apoptotic compounds
 XX PS Claim 6; Pages 28-29; 31pp; English.
 XX CC This represents the amino acid sequence of a MORT1 isoform MORT1del21.
 CC The encoding cDNA was isolated from human brain and deposited under the
 CC accession number ATCC 209018. The cDNA has a 21 base pair deletion as
 CC compared to the published MORT1 sequence (Op 172-192 of the coding
 CC sequence). The invention relates to three MORT1 nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the

CC death domain of Fas/AP01. The MORT1 isoforms can also interact with MACH
 CC alpha1 or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.
 XX SQ Sequence 201 AA;
 Query Match 75.7%; Score 985.5; DB 20; Length 201;
 Best Local Similarity 95.7%; Pred. No. 5.5e-93;
 Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
 QY 49 MDPFLVLLHSVSSSSSELTEKLCGRVVKRKLKRVQSGDLDFSMLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslseseltelkclgrvgrkrlervqsgdlfsmleqndlep--- 57
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAPGEEDLCAAFNVICDNVKGDKWRRLARQLK 168
 DB 58 ----ellaalrrhdlrrvddfeagaaagapgeedlcaafnvicdnvkgdkwrrlarqlk 113
 QY 169 VSDTKIDSTEDRYPRNLTERVRESLRWKTEKENATVAHLVGLRSCOMNLVADLVQEV 228
 DB 114 vadtksiedryprnltervreslrwktekenatvahlvglrscqmnlaadlvgev 173
 QY 229 QOARDLQNRSGAMSPMSWNSDASTSEAS 256
 DB 174 qqardlqnrsgamspmswnsdastseas 201
 RESULT 10
 AAW87491
 ID AAW87491 standard; Protein; 201 AA.
 XX AC AAW87491;
 XX DT 12-FEB-1999 (first entry)
 XX DE Amino acid sequence of MORT1 isoform MORT1del21 from NTERA2 cells.
 KW MORT1; MORT1del21; NTERA2; CNS; isoform; death domain; Fas/AP01;
 KW MACH alpha1; ICE/Ced3; caspase; anti-apoptotic; gene therapy;
 KW in vivo agent; neuronal apoptosis; human.
 XX OS Homo sapiens.
 XX PN WO9849297-A1.
 XX PD 05-NOV-1998.
 XX PF 14-APR-1998; 98WO-US07439.
 XX PR 25-APR-1997; 97US-0044835.
 XX PA (AMHP) AMERICAN HOME PROD CORP.
 XX PI Bingham BW, Birsan C, Wood AT, Young KH;
 XX DR WPI; 1999-009424/01.
 XX DR N-PSDB; AAV71928.
 XX PT Human, neuronal MORT1 isoform(s) - used as screening agents in
 XX PT diagnosing CNS diseases, and in discovering CNS-specific
 XX PT anti-apoptotic compounds
 XX PS Claim 5; Pages 26-27; 31pp; English.
 XX CC This represents the amino acid sequence of a MORT1 isoform MORT1del21.
 CC The encoding cDNA was isolated from NTERA2 cells and deposited under the
 CC accession number ATCC 209013. The cDNA has a 21 base pair deletion as

Sun Aug 18 12:47:10 2002

CC compared to the published MORR1 sequence (bp 172-192 of the coding
 CC sequence). The invention relates to three MORR1 nucleic acid isoforms
 CC (AAV71928 to AAV71930) that encode proteins which can interact with the
 CC death domain of Fas/AP01. The MORR1 isoforms can also interact with NACH
 CC alpha or other members of the ICE/Ced3 (Caspase) family of proteins.
 CC The transcript isoforms, together with their encoded proteins are useful
 CC as screening agents in diagnosing CNS diseases, and in discovering CNS-
 CC specific anti-apoptotic compounds. They are useful in gene therapy
 CC either as in vivo agents in humans or as experimental tools in
 CC manipulating neuronal apoptosis in cell culture and animal model
 CC systems.

XX Sequence 201 AA;
 SQ

Query Match 75.5%; Score 982.5; DB 20; Length 201;
 Best Local Similarity 95.7%; Pred. No. 11e-92;
 Matches 199; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTTELKFLCLGRVYVKKLRRVQSGDLFSMLLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslsseeltelkflclgrvyrkrklervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDNGKDWRRRLARQLK 168
 DB 58 ----ellaslrrhdlrrvddfeagaaagaeedlcaafnvicdngkdwrrrlarqlk 113
 QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
 DB 114 vsdtkidsiedryprnltervreslriwntekenatvahlgalscomnlvadlvqev 173
 QY 229 QOARDLQNRGAMSPMSWNSDASTSEAS 256
 DB 174 qoardlqnrsgamspmswnsdastseas 201

RESULT 11
 AAB61900
 ID AAB61900 standard; Protein: 205 AA.
 AC AAB61900;
 XX
 DT 08-MAY-2001 (first entry)
 DE Mouse apoptosis mediator FADD.
 XX FADD; DED; FADD-DED; death effector domain; apoptosis mediator;
 KW bacterial; cell death; reactive oxygen species; ROS; mouse.
 XX Mus sp.
 XX W020104153-A1.
 XX 18-JAN-2001.
 XX 11-JUL-2000; 2000WO-KR00721.
 XX 12-JUL-1999; 99KR-0027964.
 XX (IMAG-) IMAGENE CO LTD.
 XX Kim S, Kim K;
 XX WPI; 2001-138318/14.
 DR N-PSDB; AAC85064.
 XX Novel death effector domain of mammalian apoptosis mediator, for
 PT inducing bacterial and mammalian cell death by enhancing cellular level
 PT of reactive oxygen species
 XX Claim 1; Page 43-44; 47pp; English.
 XX The invention relates to a death effector domain (DED) of a mammalian

CC apoptosis mediator (FADD). The FADD-DED induces bacterial and mammalian
 CC cell death by enhancing cellular level of Reactive Oxygen Species (ROS).
 CC The present sequence represents a mouse FADD, a pro-apoptotic mediator
 CC consisting of N-terminal death effector domain (DED) and C-terminal death
 CC domain (DD).
 XX Sequence 205 AA;
 SQ

Query Match 55.3%; Score 719.5; DB 22; Length 205;
 Best Local Similarity 68.4%; Pred. No. 1.2e-65;
 Matches 141; Conservative 34; Mismatches 28; Indels 3; Gaps 1;

QY 49 MDPFLVLLHSVSSLSSELTTELKFLCLGRVYVKKLRRVQSGDLFSMLLEQNDLEPGHT 108
 DB 1 mdpflvllhsvsslsseeltelkflclgrvyrkrklervqsgldlfsmlleqndlepght 60
 QY 109 ELLRELLASLRHDLRRVDDFEAGAAAGAEEDLCAAFNVICDNGKDWRRRLARQLK 168
 DB 51 glirellaslrrhdlrrvddfeagaaagaeedlcaafnvicdngkdwrrrlarelk 120
 QY 169 VSDTKIDSIEDRYPRNLTERVRESLRIMKTEKENATVAHLVGALRSCOMNLVADLVQEV 228
 DB 121 vseakmdgieekyprlservreslriwntekenatvahlgalscomnlvadlvqev 180
 QY 229 QOARDLQNRGAMSPMSWNSDASTSE 254
 DB 181 qes---vaksenmgsplrdstvsse 203

RESULT 12
 AAB84800
 ID AAB84800 standard; Protein: 83 AA.
 AC AAB84800;
 XX
 DT 12-JUL-2001 (first entry)
 DE FADD death effector domain 1.
 XX NF-kappaB; JNK; apoptosis; death effector domain; DED.
 KW Homo sapiens.
 XX US6207458-B1.
 XX 27-MAR-2001.
 XX 07-MAY-1998; 98US-0074044.
 XX 07-MAY-1998; 98US-0074044.
 XX (UNIW) UNIV WASHINGTON.
 XX Chaudhary PM, Hood L;
 XX WPI; 2001-342087/36.
 XX Testing candidate compound affecting cellular NF-kappaB JNK, apoptosis
 PT activity by comparing cell activity in presence and absence of
 PT proteinaceous species having two death effector domain and test
 PT compound -
 XX Claim 10; Column 45-47; 62pp; English.
 XX The present invention relates to testing candidate compounds to
 CC determine whether they affect NF-kappaB, JNK and apoptosis activity.
 CC The method involves the use of 2 death effector domains (DED). The
 CC compounds identified by the invention have therapeutic
 CC applications and are useful for regulating cellular NF-kappaB, JNK
 CC and apoptosis activity. The assay is useful for identifying
 CC pharmacological agents or lead compounds generally involved in
 CC assaying for compounds which regulate or modulate a cell activity.

CC The present sequence is a death effector domain of the invention.

XX Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 1.8e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTTELKFLCLGRVYVVKRLERVQSGDLDFSMLEQNDLEPGHT 108
DB 1 mdplvllhsvsslssesttelkflclgrvgrkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDDFE 131
DB 61 ellrellaslrhdlrrvddfe 83

RESULT 13

AAB61115
ID AAB61115 standard; protein; 83 AA.

XX AAB61115;

DT 02-MAY-2001 (first entry)

DE Human FADD DED1 domain.

KW Human; FADD; apoptotic; nuclear factor-kappa B; NF-kB;
KW Jun N-terminal kinase; JUNK; apoptosis; Caspase-8 mutant;
KW death effector domain; DED.

XX Homo sapiens.

PN US6160095-A.

PD 12-DEC-2000.

PF 24-AUG-1999; 99US-0382155.

PR 07-MAY-1998; 98US-0074044.

PA (UNIW) UNIV WASHINGTON.

PI (STOW) STOWERS INST MEDICAL RES.

PI Hood L, Chaudhary PW;

XX WPI; 2001-101569/11.

XX Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT for therapeutic purposes -

PS Example 8; Fig 11; 60pp; English.

XX The present sequence is a death effector domain (DED) of a protein
CC that has been shown to regulate the nuclear factor-kappa
CC B (NF-kB), Jun N-terminal kinase (JUNK) and apoptosis pathways. It
CC is provided in a specification relating to novel mutants (D73A, L74A and
CC L75A) for Caspase-8, which are also useful for regulating NF-kB, JUNK
CC and apoptosis activities. The Caspase-8 mutants are useful for
CC therapeutic purposes and in test methods or assays for determining
CC whether a candidate compound has a significant effect upon cell
CC activities, especially NF-kB, JUNK and apoptosis, so as to facilitate the
CC discovery and/or design of therapeutic agents.

XX Sequence 83 AA;

Query Match 30.8%; Score 401; DB 22; Length 83;
Best Local Similarity 98.8%; Pred. No. 1.8e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTTELKFLCLGRVYVVKRLERVQSGDLDFSMLEQNDLEPGHT 108
DB 1 mdplvllhsvsslssesttelkflclgrvgrkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDDFE 131
DB 61 ellrellaslrhdlrrvddfe 83

RESULT 14

AAW76623
ID AAW76623 standard; protein; 81 AA.

XX AAW76623;

DT 12-JUL-1999 (first entry)

DE Human FADD protein fragment containing death effector domain.

KW Death effector domain; human; murine; anti-apoptotic; treatment;
KW HIV infection; autoimmune disease; FADD protein.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 6 /label= unknown

XX DE19713393-A1.

PN 08-OCT-1998.

PD 01-APR-1997; 97DE-1013393.

PF 01-APR-1997; 97DE-1013393.

PR (TSCH/) TSCHOPP J.

PA (APOT-) APOTTECH SA.

XX Bodmer J, Burns K, French EL, Hahne M, Hoffmann K;
PI Irmeler M, Rimoldi D, Schneider P, Schroeter M, Steiner V;
PI Thome M, Tschoopp J, Hofmann K;

XX WPI; 1998-532710/46.

XX New DNA encoding for anti-apoptotic gene product - used to treat HIV
PT infections and autoimmune diseases

XX Disclosure; Fig 2; 45pp; German.

XX This invention describes novel human and mouse anti-apoptotic gene
CC products which contain at least one death effector domain. The products
CC of the invention are used in the treatment of HIV infections and
CC autoimmune diseases.

XX Sequence 81 AA;

Query Match 28.8%; Score 375; DB 19; Length 81;
Best Local Similarity 95.1%; Pred. No. 8.1e-31;
Matches 77; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 49 MDPLVLVHVSLSSELTTELKFLCLGRVYVVKRLERVQSGDLDFSMLEQNDLEPGHT 108
DB 1 mdplvllhsvsslssesttelkflclgrvgrkrklervqsgldlfsmlleqndlepght 60
QY 109 ELLRELLASLRHDLRRVDD 129
DB 61 ellrellaslrhdlrrvdd 81

RESULT 15

AAB61902

Sun Aug 18 12:47:09 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 00:39:00 ; Search time 54.76 Seconds
(without alignments)
7630.069 Million cell updates/sec

Title: US-09-824-134-1
Perfect score: 1701
Sequence: 1 GTGAATCAGGACCGGAGTG.....ACAAAAA.....AAAAA 1701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCPUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1701	100.0	1701	3	US-09-357-072-1
2	1701	100.0	1701	5	US-09-357-072-1
3	1701	100.0	1701	5	US-09-357-072-1
4	620.6	36.5	627	4	US-09-064-414-5
5	571.8	33.6	606	4	US-09-064-414-1
6	570.2	33.5	606	4	US-09-064-414-3
7	52.6	3.1	68750	3	US-09-335-409-1
8	52.6	3.1	68750	4	US-09-335-409-1
9	52.6	3.1	68750	4	US-09-568-486-1
10	52.6	3.1	68750	4	US-09-568-486-1
11	52.6	3.1	68750	4	US-09-568-486-1
12	52.6	3.1	68750	4	US-09-568-486-1
13	50	2.9	11219	3	US-07-642-734C-1
14	50	2.9	11219	3	US-08-439-009A-1
15	49.6	2.9	2961	2	US-08-407-875-1
16	49.4	2.9	5437	1	US-07-661-610C-1
17	49.2	2.9	30001	2	US-08-125-468-1
18	49.2	2.9	30001	2	US-08-474-933-1
19	49	2.9	1777	2	US-08-173-508-5
20	49	2.9	1777	2	US-08-265-310-5
21	49	2.9	1777	3	US-08-951-742-5
22	49	2.9	2635	3	US-09-126-280-1
23	49	2.9	2670	3	US-09-126-280-1
24	48.4	2.8	4695	2	US-08-231-193A-57
25	48.4	2.8	4695	2	US-08-486-273A-57
26	48.4	2.8	4695	3	US-08-940-086A-57
27	48.4	2.8	4695	4	US-08-940-035A-57

28	47.8	2.8	1764	4	US-08-980-832-36	Sequence 36, Appl
29	47.6	2.8	2670	3	US-09-126-280-1	Sequence 1, Appl
30	47.4	2.8	2961	2	US-08-407-875-1	Sequence 1, Appl
31	47.4	2.8	68750	3	US-09-335-409-1	Sequence 1, Appl
32	47.4	2.8	68750	4	US-09-568-102-1	Sequence 1, Appl
33	47.4	2.8	68750	4	US-09-567-969-1	Sequence 1, Appl
34	47.4	2.8	68750	4	US-09-568-480-1	Sequence 1, Appl
35	47.4	2.8	68750	4	US-09-568-486-1	Sequence 1, Appl
36	47.4	2.8	68750	4	US-09-568-472-1	Sequence 1, Appl
37	47.2	2.8	1489	4	US-09-487-445-10	Sequence 10, Appl
38	46.8	2.8	20235	1	US-07-642-734C-3	Sequence 3, Appl
39	46.8	2.8	20235	3	US-08-439-009A-3	Sequence 3, Appl
40	46.6	2.7	30001	1	US-08-125-468-1	Sequence 1, Appl
41	46.6	2.7	30001	2	US-08-474-933-1	Sequence 1, Appl
42	46.2	2.7	2580	3	US-09-050-863-2	Sequence 2, Appl
43	46.2	2.7	2580	4	US-09-359-081-2	Sequence 2, Appl
44	46.2	2.7	5452	2	US-09-130-114-1	Sequence 1, Appl
45	46.2	2.7	9600	4	US-08-910-647-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-357-072-1
; Sequence 1, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 1
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(771)
US-09-357-072-1

Query Match	100.0%	Score	1701	DB	3	Length	1701
Best Local Similarity	100.0%	Pred. No.	0	Mismatches	0	Indels	0
Matches	1701	Conservative	0	0	0	Gaps	0
Qy	1	GTGAATCAGGACCGGAGTGCGAGTTCGGGGTGGAAATCCTTGGCGCGTGGCGAAGCGG	60				
Db	1	gtgaatcaggcagcgagtgctgggggtggaaatccttggcgcggtggcgcgagcgagcgag	60				
Qy	61	CGAGACCTGGCCAGGCGGACGAGCCGAGGACAGAGGCGGCGGAGGCGGCGGCGGCGG	120				
Db	61	cgaagctggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag	120				
Qy	121	CCCCGGCGCTTGAGACCCCGCCATGACCGCTCTGGTGTCTGCTGCTGCTGCTGCTGCTG	180				
Db	121	ccccggcgcttgagagcccgccatggagccgcttccttggtgctgctgctgctgctgctg	180				
Qy	181	TCCAGCCTGTGAGAGGAGGAGCTGACCGAGCTCAAGTTCCTATGCTGCGGCGGCTGCTC	240				
Db	181	tcagcctgtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	240				
Qy	241	AAGCCGAAGTGGAGCGGCTGAGAGCGGCTAGACCTTCTTCTCATGCTGCTGAGCAG	300				
Db	241	aagcgaagctggagcgctgagagcgagcgagcgagcgagcgagcgagcgagcgagcgag	300				
Qy	301	ACGACCTGAGCGCGGCGACACCGAGCTCTGCGCGAGCTGCTGCGCTCCCTCGGCGGC	360				
Db	301	acgacctgagcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag	360				

[illegible]

RESULT 2
PCT-US95-16542-1
: Sequence 1, Application PC/TUS9516542
: GENERAL INFORMATION:
: APPLICANT: YEDA RESEARCH AND DEVELOPMENT CO. LTD.
: APPLICANT: WEINURZEL, Henry
: APPLICANT: WOLLACH, David
: APPLICANT: BOLDIN, Mark
: APPLICANT: VARFOLOMEYEV, Eugene
: APPLICANT: METT, Igor
: TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APOLI
: TITLE OF INVENTION: RECEPTORS
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street N.W., Ste..300
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States of America
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION NUMBER: PCT/US95/16542
: APPLICATION DATA:
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 112022
: FILING DATE: 15-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 112692
: FILING DATE: 19-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 114615
: FILING DATE: 16-JUL-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-16
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: TELEX: 248633
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1701 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..768
PCT-US95-16342-1

Query Match
Best Local Similarity 100.0%; Score 1701; DB 5; Length 1701;
Matches 1701; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GTGAATCAGGACCGGAGTTCGCGGGTGGGAATCCTTGGGCGCTGGGCAAGCGG 60
Db 1 GTGAATCAGGACCGGAGTTCGCGGGTGGGAATCCTTGGGCGCTGGGCAAGCGG 60
QY 61 CGAGACCTGGCCAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 61 CGAGACCTGGCCAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 121 CCCGCGCGCTTGCAGACCCCGCCATGGACCGTTCCTGGTGTCTGTGCTGCTG 180
Db 121 CCCGCGCGCTTGCAGACCCCGCCATGGACCGTTCCTGGTGTCTGTGCTGCTG 180
QY 181 TCCAGCCTGTTCGAGCAGCGAGTGCACGAGCTCAAGTTTCCTATGCCGCGGCGG 240
Db 181 TCCAGCCTGTTCGAGCAGCGAGTGCACGAGCTCAAGTTTCCTATGCCGCGGCGG 240
QY 241 AAGCGCAAGCTGGAGCGGCTGCAGAGCGGCTAGACCTCTTCCATGTCTGGAGCAG 300
Db 241 AAGCGCAAGCTGGAGCGGCTGCAGAGCGGCTAGACCTCTTCCATGTCTGGAGCAG 300
QY 301 AACGACCTGGAGCGGCGGACACGAGCTCCTGCGGAGCTGCTGCGCTCCTTCCATGTCTGGAGCAG 360
Db 301 AACGACCTGGAGCGGCGGACACGAGCTCCTGCGGAGCTGCTGCGCTCCTTCCATGTCTGGAGCAG 360
QY 361 CACGACCTGCTGCGGCGGCTGCAGAGCTTCGAGCGGCGGCGGCGGCGGCGGCG 420
Db 361 CACGACCTGCTGCGGCGGCTGCAGAGCTTCGAGCGGCGGCGGCGGCGGCGGCG 420
QY 421 GGGGAAGAACCTGTGTGAGGATTTACGTCATATGTGTAATGTGGGAAAGATTGG 480
Db 421 GGGGAAGAACCTGTGTGAGGATTTACGTCATATGTGTAATGTGGGAAAGATTGG 480
QY 481 AGAAGCTGCTGCTCAGCTCAAGTCTCAGACACCAAGATCGACAGATCGAGGACAG 540
Db 481 AGAAGCTGCTGCTCAGCTCAAGTCTCAGACACCAAGATCGACAGATCGAGGACAG 540
QY 541 TACCCCGCAACCTGACAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 600
Db 541 TACCCCGCAACCTGACAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 600
QY 601 AAGGAGAACGCAACAGTGGCCCGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 660
Db 601 AAGGAGAACGCAACAGTGGCCCGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 660
QY 661 GTGGCTGACCTGTGACAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 720
Db 661 GTGGCTGACCTGTGACAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 720
QY 721 ATGTCCCGATGTCATGGAAGCTCAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 780
Db 721 ATGTCCCGATGTCATGGAAGCTCAGAGGCTGCGGAGCTCAGTGAATCTGGAAGAACACAGAG 780
QY 781 GCTTTGGCGTGGTGGACCAAGCTATACAGGCTGAGCTTTGGTTCTTCCAGGAAG 840
Db 781 GCTTTGGCGTGGTGGACCAAGCTATACAGGCTGAGCTTTGGTTCTTCCAGGAAG 840
QY 841 GTAGCCAGCACTGTGAAGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 841 GTAGCCAGCACTGTGAAGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 CTTCTGAAGTCAAGCTGGTTTATTAATGCCTCTCTCCCGCAGGCGGCGCTGGGCGCT 960

Db 901 CTTCTGAAGTCAAGCTGGTTTATTAATGCCTCTCTCCCGCAGGCGGCGCTGGGCGCT 960
QY 961 GCACAGATATTTCCATTCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1020
Db 961 GCACAGATATTTCCATTCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1020
QY 1021 TGAGTCTCTGCGGAGTAGTTGGAAAGTTGGAAAGTTGGAAAGTTGGAAAGTTGG 1080
Db 1021 TGAGTCTCTGCGGAGTAGTTGGAAAGTTGGAAAGTTGGAAAGTTGGAAAGTTGG 1080
QY 1081 CAGATGACGAGTACACCTGTTTACTCCACGCGGAGGAGGAGGAGGAGGAGGAGG 1140
Db 1081 CAGATGACGAGTACACCTGTTTACTCCACGCGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 CGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db 1141 CGGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 CCATGCTCAACCACTGTGGCGTCTGCTCCCTTGCAGTTGGCAGAAAGGATGTTTTGT 1260
Db 1201 CCATGCTCAACCACTGTGGCGTCTGCTCCCTTGCAGTTGGCAGAAAGGATGTTTTGT 1260
QY 1261 CCATTTCTTGGAGCGCCACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1261 CCATTTCTTGGAGCGCCACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1321 GTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Db 1321 GTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 TGGCCCTGTGAGGATGAGTCTCTCTGAGACTGCTAAGTAGGGGAGGAGTGTGTTG 1440
Db 1381 TGGCCCTGTGAGGATGAGTCTCTCTGAGACTGCTAAGTAGGGGAGGAGTGTGTTG 1440
QY 1441 CCAGGAGAAATGAGATAATATCTGAGGAGTCTGATGAGTGTGATGACACAGCACTCT 1500
Db 1441 CCAGGAGAAATGAGATAATATCTGAGGAGTCTGATGAGTGTGATGACACAGCACTCT 1500
QY 1501 CTAAATCTCTCTGAGGATGAGTCTGCAATTTCTACAGTTTCTTACTGTTTGA 1560
Db 1501 CTAAATCTCTCTGAGGATGAGTCTGCAATTTCTACAGTTTCTTACTGTTTGA 1560
QY 1561 TCAAAATCACTATCTTCTGATAACAGAAATTCGCAAGGAGGAGGAGTCTGATCTTTAA 1620
Db 1561 TCAAAATCACTATCTTCTGATAACAGAAATTCGCAAGGAGGAGGAGTCTGATCTTTAA 1620
QY 1621 AAAGCAGTCTCTTATTTCTGATAACAGAAATTCGCAAGGAGGAGGAGTCTGATCTTTAA 1680
Db 1621 AAAGCAGTCTCTTATTTCTGATAACAGAAATTCGCAAGGAGGAGGAGTCTGATCTTTAA 1680
QY 1681 TACAAAAAATAAAAAAAAAA 1701
Db 1681 TACAAAAAATAAAAAAAAAA 1701

RESULT 3
PCT-US96-10521-1
; Sequence 1, Application PC/TUS9610521
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 114.615
;; FILING DATE: 16-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 114.986
;; FILING DATE: 17-AUG-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 115.319
;; FILING DATE: 14-SEP-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 116.588
;; FILING DATE: 27-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: IL 117.932
;; FILING DATE: 16-APR-1996
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1701 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..768
PCT-US96-10521-1

Query Match 100.0%; Score 1701; DB 5; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAATCAGGCGGAGCTGCGAGTTGGGGTGAATCCTTGGGCGCTGGGCAAGCGG 60
DB 1 GTGAATCAGGCGGAGCTGCGAGTTGGGGTGAATCCTTGGGCGCTGGGCAAGCGG 60
QY 61 CGAGACTGGCGGCGGAGCGGAGCGGAGGAGGCGGCGGCGGCGGCGGCGAG 120
DB 61 CGAGACTGGCGGCGGAGCGGAGCGGAGGAGGCGGCGGCGGCGGCGGCGAG 120
QY 121 CCCGGCGGCTTGCAGACCCCGCATGACCGCTTCTGCTGCTGCTGCTGCTGCTG 180
DB 121 CCCGGCGGCTTGCAGACCCCGCATGACCGCTTCTGCTGCTGCTGCTGCTGCTG 180
QY 181 TCCAGCTGTGCGAGCGGAGCTGACGAGCTCAAGTTCCTATGCTCGGCGCGTGGTC 240
DB 181 TCCAGCTGTGCGAGCGGAGCTGACGAGCTCAAGTTCCTATGCTCGGCGCGTGGTC 240
QY 241 AAGCGCAAGCTGGAGCGCTGCGAGCGGCGCTAGACCTCTTCTCCATGCTGTGGAGCAG 300
DB 241 AAGCGCAAGCTGGAGCGCTGCGAGCGGCGCTAGACCTCTTCTCCATGCTGTGGAGCAG 300
QY 301 AAGCGCTGGAGCGGCGGCGGCGGAGCTCTGCGGAGCTGCTGCGCTCCCTGCGGCGC 360
DB 301 AAGCGCTGGAGCGGCGGCGGCGGAGCTCTGCGGAGCTGCTGCGCTCCCTGCGGCGC 360
QY 361 CAGGACTGCTGCGGCGCTCGAGCGCTTCGAGCGGCGGCGGCGGCGGCGGCGGCGCT 420
DB 361 CAGGACTGCTGCGGCGCTCGAGCGCTTCGAGCGGCGGCGGCGGCGGCGGCGGCGCT 420
QY 421 GGGGAAGAAGCTGTGTGAGCATTAAAGTTCATATGTGATAATGTGGGAAGATTGG 480
DB 421 GGGGAAGAAGCTGTGTGAGCATTAAAGTTCATATGTGATAATGTGGGAAGATTGG 480
QY 481 AGAAGGCTGGCTGCTGAGCTCAAGCTCAGACCAAGATCGACAGATCGAGGACAGA 540
DB 481 AGAAGGCTGGCTGCTGAGCTCAAGCTCAGACCAAGATCGACAGATCGAGGACAGA 540
QY 541 TACCCCGCAACCTGACAGAGCGTGTGGGAGTCACTGAGAACTGGAAGAACACAGAG 600
DB 541 TACCCCGCAACCTGACAGAGCGTGTGGGAGTCACTGAGAACTGGAAGAACACAGAG 600
QY 601 AAGGAGAGCGCAACAGTGGCCACCTGTGTGGGGCTCTCAGGCTCTGCCAGATGAACCTG 660

DB 601 AAGGAGAACCAACAGTGGCCACCTGGTGGGGCTCTCAGGCTCTGCCAGATGAACCTG 660
QY 661 GTGGCTGACCTGTGTACAGAGTTTACAGAGCCCGTGTGACTCTCAGAACAGGAGTGGGGC 720
DB 661 GTGGCTGACCTGTGTACAGAGTTTACAGAGCCCGTGTGACTCTCAGAACAGGAGTGGGGC 720
QY 721 ATGTCCCGATGTCTATGGAACTCAGACGATCTTACCTCCGAAGCGTCTGTATGGCCGCT 780
DB 721 ATGTCCCGATGTCTATGGAACTCAGACGATCTTACCTCCGAAGCGTCTGTATGGCCGCT 780
QY 781 GCTTTGGCTGTGGACACAGCATCTACAGCGCTTGACTTTGTTCTCTCCAGAGAG 840
DB 781 GCTTTGGCTGTGGACACAGCATCTTACAGCGCTTGACTTTGTTCTCTCCAGAGAG 840
QY 841 GTAGCCGACACTGTGAGACCCAGCAGGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGCTG 900
DB 841 GTAGCCGACACTGTGAGACCCAGCAGGAGCCAGAGCCAGAGCCAGAGCCAGAGCCAGCTG 900
QY 901 CTTCTGAACCTCAAGCTGGCTTTTATTAATGCTCTCCCGACCCAGCGCGGCTGGGCCCT 960
DB 901 CTTCTGAACCTCAAGCTGGCTTTTATTAATGCTCTCCCGACCCAGCGCGGCTGGGCCCT 960
QY 961 GCACAGATATTTCCATTTCTTCTCCTCATATGACACTGAGCAGATCTTGTCTCCACTAAA 1020
DB 961 GCACAGATATTTCCATTTCTTCTCCTCATATGACACTGAGCAGATCTTGTCTCCACTAAA 1020
QY 1021 TGAGCTCTCGGGAGTGTGGAAAGTTGGAACCGTGTCCAGCAGACAGAAATCTGTG 1080
DB 1021 TGAGCTCTCGGGAGTGTGGAAAGTTGGAACCGTGTCCAGCAGACAGAAATCTGTG 1080
QY 1081 CAGATGAGCAGTCAACACTGTTACTCCACAGCGGAGGAGACAGCTCAGAGCCAGGAAT 1140
DB 1081 CAGATGAGCAGTCAACACTGTTACTCCACAGCGGAGGAGACAGCTCAGAGCCAGGAAT 1140
QY 1141 CGGAGCGAAGCAGAGAGTGGAGAACTGGGATTTGAACCCCGCCATCTTCCACAGAGC 1200
DB 1141 CGGAGCGAAGCAGAGAGTGGAGAACTGGGATTTGAACCCCGCCATCTTCCACAGAGC 1200
QY 1201 CCATGCTCAACACTGTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 CCATGCTCAACACTGTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CCCATTTCTTGGAGGCGACCGGAGACCTTGAGACTAGGCTCAGGCGGCGTGTGCTG 1320
DB 1261 CCCATTTCTTGGAGGCGACCGGAGACAGCTTGAGACTAGGCTCAGGCGGCGTGTGCTG 1320
QY 1321 GTGGGAGAGGAGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1380
DB 1321 GTGGGAGAGGAGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1380
QY 1381 TGGCCCTGTGTGAGTTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGCTG 1440
DB 1381 TGGCCCTGTGTGAGTTGAGTCTCTCTGAGACTGCTAAGTAGGGGAGTGTGCTG 1440
QY 1441 CCAGGAGCAATTCAGATAATATCTGTGAGTGTGTGATGATGATGATGATGATGATGAT 1500
DB 1441 CCAGGAGCAATTCAGATAATATCTGTGAGTGTGTGATGATGATGATGATGATGATGAT 1500
QY 1501 CTAATCTTCTTGTGAGGATATGGTCTGCAATTTCTACAGTTCTTACTGTTTGTGA 1560
DB 1501 CTAATCTTCTTGTGAGGATATGGTCTGCAATTTCTACAGTTCTTACTGTTTGTGA 1560
QY 1561 TCAATCACTATCTTCTTCTGATAACAGAAATGCAAGGAGCGGAGTCTCGTATCTTAA 1620
DB 1561 TCAATCACTATCTTCTTCTGATAACAGAAATGCAAGGAGCGGAGTCTCGTATCTTAA 1620
QY 1621 AAGCAGTCTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
DB 1621 AAGCAGTCTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
QY 1681 TACAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1701


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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-102-1

Query Match      3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred.No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps

QY 109 GCCGGCGCCGACGCCCGCGCTTCAGACACCCCGCATGGACCCTTCTGTGCTGCTG 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3985 ggcgctgcgccgctggcggtgcgcgcagcgcgtccctggcgcgcgaattctgtg 4044
QY 169 CACTCGGTGTCGTCAGCCTGTCGAGCAGAGTGACCGAGCTCAAGTTCTATGCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcatggttctcgtcggcgcggtcacccaactcgcgatgcgtgggtggcgcacgcg 4104
QY 229 GGCGCGCTGGTCAACGCCAAGCTGGAGCGGTGTCAGAGCGGCTAGACCTCTTCTCCATG 288
    ||||| |||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4105 acgcgcgttccaaggagcagtgtcgtcgtcgtcctcactcagttcctggcgcgcgcg 4164
QY 289 CTGCTGGAGCAGACGACCTTGAGCCCGCGGCACACCGAGCTCCTCGCGAGCTGCTCGCC 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4165 ctgacgcgcgcgtcgcgtgcacctgtcgtcgcgcgttcgcgtcgcgtcgtcgtc 4224
QY 349 TCCCTGCGGCCGCCACGACCTGCTCGCGCGGTGCGAGACTTCGAGCGGGCGCGCGGCC 408
    ||||| |||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4225 aaacgcgtcctctcgaccacacccctctcctgcgcgcgtgcgcgcgcgtgcgcgcgcg 4284
QY 409 GGGCGCGCGCGCTGGG 423
    ||||||| |
Db 4285 cttcttcgcgcctgtg 4299

RESULT 9
US-09-567-969-1
; Sequence 1, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-305B2A
; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-567-969-1

Query Match      3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred.No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps

QY 109 GCCGGCGCCGACGCCCGCGCTTCAGACACCCCGCATGGACCCTTCTGTGCTGCTG 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3985 ggcgctgcgccgctggcggtgcgcgcagcgcgtccctggcgcgcgaattctgtg 4044
QY 169 CACTCGGTGTCGTCAGCCTGTCGAGCAGAGTGACCGAGCTCAAGTTCTATGCCTC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcatggttctcgtcggcgcggtcacccaactcgcgatgcgtgggtggcgcacgcg 4104
QY 229 GGCGCGCTGGTCAACGCCAAGCTGGAGCGGTGTCAGAGCGGCTAGACCTCTTCTCCATG 288
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Db	4105	aagcggggtctccaaaggaacagggtgcctgcctcgccctcctcagcttctgcgcgcggc	4164
QY	289	CTGCTGGAGCAGAACACCTGTGAGCCGCGGCACACCGAGCTCCCTGCGGACCTGCTGCC	348
Db	4165	ctgacgcagcggctgcggcctgcacscgtctgctcggcgcggttcgcgctcggcgtgctgc	4224
QY	349	TCCTCTGGCGGGCCACACACCTGTGCGGGCGCTCGACGACTTCGAGCGGGGGCGCGGCC	408
Db	4225	aacagcgctctctgcaccacacccctctctctcgcacggtgcgcagacgctcgtggcgggc	4284
QY	409	GGGGCGCGCCTGGG	423
Db	4285	ctcttcgcgcctatg	4299

RESULT 10
 US-09-568-480-1
 ; Sequence 1, Application US/09568480
 ; Patent No. 6355458
 ; GENERAL INFORMATION:
 ; APPLICANT: Schupp, Thomas
 ; APPLICANT: Ligon, James
 ; APPLICANT: Molnar, Istvan
 ; APPLICANT: Zirkle, Ross
 ; APPLICANT: Cyr, Devon
 ; APPLICANT: Goerlach, Joern
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 ; FILE REFERENCE: 4-30582A
 ; CURRENT APPLICATION NUMBER: US/09/568,480
 ; CURRENT FILING DATE: 2000-05-10
 ; PRIOR APPLICATION NUMBER: 09/335,409
 ; PRIOR FILING DATE: 1999-06-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 68750
 ; TYPE: DNA
 ; ORGANISM: Sorangium cellulosum
 US-09-568-480-1

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Query Match      3.1%: Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGGCGCAGCCCCCGCGCTTGACAGACCCCGCATGGACCGCTTCTCGGTGCTGCTG 168.
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3985 ggcgcgtccgcgcgtcggcggtcgcccgagcgcctctcgagcgagattttgtg 4044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 CACTCGGTGCGTCCAGCGCTGTGCAGACGCGAGTGACCGAGCTCAAGTTCTATGCCTC 228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4045 ttcatggctcgtcggcgcgctcaccacactcgatcgcgctgggtggccgacgcg 4104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 229 GGGCGCGTGTCAAGCGCAAGCTGGAGCGCGTGCGAGCGGCCTAGACCTTTCTTCATG 288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4105 acgcgcgtctccaaaggacaggtgtcgtcgctcgtctcctcacgttctcgccgcgcg 4164
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 CTGTGTGAGAGAGACGACCTGTGAGCCCGGGCACACCGAGCTCTCTGCGGAGCTCGCTGCC 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4165 ctgacgcagcggctcggccctgcacccgctcgtcggcggttcgcgcctcggcgcgtc 4224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 TCCTTCGGGGCGCACGACCTGCTCGCGGCGGTGCACACTTCGAGCGGGGGGGGGCGCC 408
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4225 aacagcgtcctcgcaccaaacccctctcctcagcggtgcagacgctcgtggcggc 4284
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 409 GGGGCGCGCCTGGG 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4285 ctcttcgcgcctga 4299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 11
US-09-568-486-1

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: Sequence 1, Application US/09568486
: Patent No. 6355459
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James
: APPLICANT: Molnar, Istvan
: APPLICANT: Zirkle, Ross
: APPLICANT: Cyr, Devon
: APPLICANT: Goerlach, Joern
: TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
: FILE REFERENCE: 4-30552A
: CURRENT APPLICATION NUMBER: US/09/568,486
: CURRENT FILING DATE: 2000-05-10
: PRIOR APPLICATION NUMBER: 09/335,409
: PRIOR FILING DATE: 1999-06-17
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 68750
: TYPE: DNA
: ORGANISM: Sorangium cellulosum
: US-09-568-486-1

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Query Match	3.1%;	Score	52.6;	DB	4;	Length	68750;
Best Local Similarity	47.9%;	Pred.	No. 0.011;				
Matches	151;	Conservative	0;	Mismatches	164;	Indels	0;
Gaps							
O:							
QY	109	GGCGGGCGCAGCCCCGCGCTTCGACAGCCGCCATCGACCCTTCTGTGTGTGTGTG	168				
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QY	169	CACCTCGGTGTGTCTCCAGCGCTGTCGAGCAGCGAGTGACCGAGCTCAAGTTCTATGCCTC	228				
Db	4045	ttoatggtgcgtcgtggcgcgcgctaccacactcgcgatgcgtggctggcgacgcgcg	4104				
QY	229	GGGCGGTGTCAACGCGAAGCTGTGAGCGCGCTGCAGAGCGGCCTTAGACCTCTTCTCCATG	288				
Db	4105	acgcgcgtctccaaaggacacagtgtgcgtcgtctcctcacgttcctggcgcgcgcg	4164				
QY	289	CTGCTGGAGCAGACGACCTTGGACCCGGGACACACCGAGTCTTCGCGAGCTCTCGCC	348				
Db	4165	ctgacgacagcgctgcggccttgcaacctgctgcgcgttcgcgcgtgcgcgtc	4224				
QY	349	TCCCTGGGGGGCCACGACCTGCTCGCGCGCGTGCAGACTTCGAGCGGGGGGGGGGCC	408				
Db	4225	aacagcgctcctgcgaccaaacccctctcctcgcagcgctgcagacgctcgtggcgggc	4284				
QY	409	GGGCGCGCGCTGGG	423				
Db	4285	ctcttcgcgcctatg	4299				

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RESULT 12
US-09-568-472-1
; Sequence 1, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568.472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
; US-09-568-472-1

Query Match      3.1%; Score 52.6; DB 4; Length 68750;
Best Local Similarity 47.9%; Pred. NO. 0.011;
Matches 151; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 109 GCCGGCGCCAGCGCGCGCTGTCAGAGCCCGCCGACACCGCCGCTGCTGCTGCTGCTG 168
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Db 3985 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 CACTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4045 ttcattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 229 GGCGCGGTGCTCAAGCGCAAGCTGGAGCGCGTGCAGAGCGCGCTAGACCTCTTCTCCATG 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4105 agcgcgcgtctcaaggagagagagagagagagagagagagagagagagagagagagag 4164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 289 CTGCTGGAGCAGAACGACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4165 ctgacgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 4224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 349 TCCTCTCGCGCGCACGACCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
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Db 4225 aacagcgcctctcgcacacacacacacacacacacacacacacacacacacacacacac 4284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 409 GGGCGCGCGCGCTGGG 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4285 ctcttcgcgcgcgtg 4299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-07-642-734C-1
; Sequence 1, Application US/07642734C
; Patent No. 5824513
; GENERAL INFORMATION:
; APPLICANT: Katz, L
; APPLICANT: Donadio, S
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Recombinant DNA Method for Producing
; TITLE OF INVENTION: Erythromycin Analogs
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward H. Gorman
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Park Rd
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 17-JAN-91
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Danckers, Andreas M
; REGISTRATION NUMBER: 32652
; REFERENCE/DOCKET NUMBER: 4952.US.01
; TELEPHONE: 708-937-9396
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11219 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharopolyspora erythraea
; STRAIN: NRRL 2338
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 744..6659
; OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
; OTHER INFORMATION: MODULE 1"
; OTHER INFORMATION: /label= FUNCTION
; NAME/KEY: CDS
; LOCATION: 744..11219
; OTHER INFORMATION: /function= "gene= "eryA"
; OTHER INFORMATION: /product= "ORF1 encoding modules 1 & 2 for
; OTHER INFORMATION: 6-deoxyerythronolide B"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 744..1868
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyltransferase domain 1 of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1998..2198
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyl carrier domain 1 of module 1"
; FEATURE:
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; LOCATION: 2250..3626
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3831..4811
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyltransferase 2 domain of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5574..6125
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoreductase domain of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6369..6626
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyl carrier domain 2 of module 1"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6678..11219
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: module 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6678..8066
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoacyl ACP synthase of module 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8262..9305
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyltransferase domain of module 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9906..10454
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: beta-ketoreductase domain of module 2"
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: 10707..10964
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: acyl carrier domain of module 2"
US-07-642-734C-1

Query Match      2.9%; Score 50; DB 1; Length 11219;
Best Local Similarity 46.7%; Pred. No. 0.025;
Matches 158; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY   80 GCGAGCCGAGACAGAGGGCGCGGAGGGCGGCGGCAGCCGCCCGCGCTGTGACAGCC 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   10699 GCGAGCCGCTGCGGGTGTGCGCGTCGCGAGCGAGCGGGAGCTGGTCCGCTGTGCC 10758
QY   140 CGCGACTGAGACCCTTCTTGCTGTGCTGTGCACTCGGTGTGCTCCAGCTGTGAGCAGCG 199
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   10759 GCACAGACCGCGACCGCTGTGCGCCACGACGACCGAAGCGGTGCGCGCACCGC 10818
QY   200 ACTGACCGAGCTCAAGTTCTATGCTCGGGCGCGTCAAGCGCAAGCTGGAGCGCG 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   10819 CATTCAAGAGACTCGGGTTCGACTCGTGGCGCGCTCCGGCTGCCGAACCTGCTCAAGC 10878
QY   260 TCGAGAGCGGCTAGACCTTCTTCATGCTGTGGAGCAGAAGCACTGGAGCCCGCGC 319
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   10939 TCGCCGGTTTTCTCGAGCGCGGAGCTCGGCACCGAGTCCGGGGGAGCGCGCTCGGCC 10998
QY   380 TCGACGACTTCGAGGGGGGGCGCGCGCGCGCGCGCGCGCGC 417
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Db   10999 TCGCGGGCTGAGCGGCTGGAAGCGCGCTCCCGGAG 11036

RESULT 14
US-08-439-009A-1
; Sequence 1, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; APPLICANT: Mcalpine, J B
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; NUMBER OF SEQUENCES: 27 Specific Polypeptides
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstein
; STREET: Abbott Laboratories D377/AP6D-2 One Abbott
; CITY: Park Rd
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11219 base pairs
; TYPE: nucleic acid

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 00:40:30 ; Search time 220.39 seconds
(without alignments)
13251.379 Million cell updates/sec

Title: US-09-824-134-1

Perfect score: 1701

Sequence: 1 GTGAATCAGGACCGGACTG.....ACAAAAA.....1701

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1701	100.0	1701	17	AAT30372
2	1701	100.0	1701	18	AAT61397
3	1701	100.0	1701	21	AAZ44745
4	1621.8	95.3	1642	17	AAT30397
5	1567.8	92.2	1582	20	ARX08910
6	620.6	36.5	627	20	AAV71930
7	571.8	33.6	606	20	AAV71928
8	570.2	33.5	606	20	AAV71929
9	363.8	21.4	1377	22	AAC85064
					MORT-1 cDNA. Homo
					MORT-1 coding sequ
					Human FADD DNA. H
					FADD (Fas-associat
					Human FADD protein
					MORT1 isoform MORT
					MORT1 isoform MORT
					Mouse apoptosis me

C	10	288.8	17.0	298	22	AAF90364
	11	53.6	3.2	1611	23	AA554123
	12	52.6	3.1	68750	21	AAZ55887
C	13	52.2	3.0	10732	21	AA10594
	14	51	3.0	51	22	AA131857
	15	50.8	3.0	1251	21	AA75683
	16	50.8	3.0	2257	22	AAF81751
	17	50.8	3.0	2351	20	AAV68667
	18	50.8	3.0	2842	21	AA000334
	19	50.8	3.0	2879	22	AA05820
	20	50.4	3.0	2561	22	AAH26500
	21	50.4	3.0	5560	24	AA598044
	22	50.2	3.0	2175	24	AA597190
	23	50	2.9	29879	14	AAQ46806
	24	49.8	2.9	2564	22	AA192870
	25	49.8	2.9	3038	22	AA514697
	26	49.8	2.9	53789	19	AAV21187
	27	49.6	2.9	2961	17	AAT38322
	28	49.6	2.9	109519	22	AA508693
	29	49.4	2.9	5437	12	AAQ13369
	30	49.2	2.9	2290	20	AA552228
	31	49.2	2.9	2290	22	AA521405
	32	49.2	2.9	2290	22	AA72386
C	33	49.2	2.9	30001	18	AA61016
C	34	49.2	2.9	30001	20	AA05110
	35	49.2	2.9	37856	21	AA11992
	36	49	2.9	1777	16	AAQ99368
	37	49	2.9	1777	20	AAV84067
	38	49	2.9	1777	21	AA61405
C	39	49	2.9	2635	21	AA59555
C	40	49	2.9	2670	21	AA59554
	41	48.6	2.9	2355	24	ABA90356
C	42	48.6	2.9	114955	20	AA53491
	43	48.4	2.8	4895	15	AAQ79378
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ALIGNMENTS

RESULT	1
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ID	AAT30372 standard; cDNA; 1701 BP.
XX	AC
AC	AAT30372;
XX	13-SEP-1996 (first entry)
DT	MORT-1 cDNA.
XX	MORT-1; HFI; FAS/AP01 receptor; FAS-R; tumour; cancer; HIV;
XX	mediator of receptor toxicity; gene therapy; ss.
OS	Homo sapiens.
XX	Key
FT	Location/Qualifiers
FT	1..771
FT	/*tag= a
XX	WO9618641-Al.
XX	20-JUN-1996.
XX	14-DEC-1995; 95WO-US16542.
XX	16-JUL-1995; 95IL-0114615.
XX	15-DEC-1994; 94IL-0112022.
XX	19-FEB-1995; 95IL-0112692.
XX	(WEIN/) WEINWURZEL H.
XX	(YEDA) YEDA RES & DEV CO LTD.

Human FADD mRNA.
Pseudomonas aerugin
Sorangium cellulos
Gene encoding a su
Human SNP oligonuc
Human OREX ORF1238
Human membrane 888
Nucleotide sequenc
Rice raffinose syn
Human reproductive
Rabbit low density
Human DNA for pote
Human metalloprote
eryA region of S.
Human polynucleoti
Human cDNA encodin
Amycolatopsis med
Metabotropic gluta
Micromonospora DNA
Fusaric acid reas
Protein PRO227 CDN
Human cDNA sequenc
Human PRO227 CDNA.
Total DNA sequence
S. aureofaciens DN
S. cellulosum DNA
S. lividans protea
Clone p8-2 encodin
cDNA encoding a su
RNA encoding a met
DNA encoding a met
Human polynucleoti
Human adenosine A1
Human N-methyl-D-a
Human N-methyl-D-a

PI Boldin M, Mett I, Varfolomeev E, Wallach D;
XX WPI; 1996-300569/30.
DR P-PSDB; AAR98346.
XX
XX MORT-1 protein capable of interacting with FAS-R intracellular
PT domain - useful for modulating FAS-R ligand effect on cells and
PT treating, e.g. tumour cells and HIV-infected cells
XX
XX Claim 3; Fig 4; 72pp; English.
XX
XX A cDNA clone (AAT30372) codes for MORT-1 (AAR98346) (Mediator of
CC Receptor Toxicity), also designated HFI, a novel protein that binds
CC to the intracellular domain (Fas-IC) of the Fas ligand receptor FAS-R
CC (or Fas/ Apo1), and is capable of modulating the function of Fas-R.
CC It was obtd. from HeLa cells using a yeast 2-hybrid screen and 2-hybrid
CC beta-galactosidase expression system. The cDNA can be used for produ.
CC of recombinant MORT-1 using transformed host cells. It can also be
CC used to modulate the FAS-R ligand on cells carrying an FAS-R and to
CC develop methods for the gene therapy of e.g. cancer and HIV infection.
XX
XX Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 other;
SQ
Query Match 100.0%; Score 1701; DB 17; Length 1701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GTGAATCAGGACCGGAGTTCGGGGTGGAAATCTTGGGCGGTGGCGCAAGCGG 60
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DB 61 CGAGACCTGGCGAGGCGGAGCGGAGGAGGAGGAGGCGCGGAGGCGGCGGAG 120
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QY 181 TCGAGCGTGTGAGGAGGCGGAGTTCAGGAGTCAAGTTCTTATGCTGCGGCGGCTGTC 240
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DB 241 AAGCGCAAGTGTGAGGCGGCTGAGGCGGCTGAGACCTTCTTCTGCTGCTGCTGCTG 300
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DB 421 GGGGAAGAGACCTGTGTCAGCATTTAAGCTCATATGTGATAATGTGCGGGAAGATTGG 480
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QY 541 TACCCCGCAACCTGACAGCGGTGCGGAGTCTGAGAGTCTGGAAGAACACAGAG 600
DB 541 TACCCCGCAACCTGACAGCGGTGCGGAGTCTGAGAGTCTGGAAGAACACAGAG 600
QY 601 AAGGAGACGCAACAGTGGCGGCGGCTGTTGGGCGGCTCTCAGGTCCTGCCAGATCAACCTG 660
DB 601 AAGGAGACGCAACAGTGGCGGCGGCTGTTGGGCGGCTCTCAGGTCCTGCCAGATCAACCTG 660
QY 661 GTGGCTGACCTGGTACAGAGAGGTTTCAGCAGGCGGCGGCTCCAGACAGGAGTGGGCGC 720

RESULT 2

AAT61397

ID AAT61397 standard; CDNA; 1701 BP.

XX AC

AAT61397;

XX DT

29-OCT-1997 (first entry)

XX DE

MORT-1 coding sequence.

XX KW

MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death; antibody; FAS ligand receptor; FAS-R; death domain region; septic shock; tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death; apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis; autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide; TNF; therapy; ss.

XX OS

Homo sapiens.

XX FH

Key Location/Qualifiers

FT CDS

1..771

/*tag= a

/product= mediator of cellular toxicity (MORT-1) protein

XX FT

W09703998-A1.

XX FN

XX PD

06-FEB-1997.

XX FF

14-JUN-1996; 96WO-US10521.

XX PR

16-APR-1996; 96IL-0117932.

XX PR

16-JUL-1995; 95IL-0114615.

XX PR

17-AUG-1995; 95IL-0114986.

XX PR

14-SEP-1995; 95IL-0115319.

XX PR

27-SEP-1995; 95IL-0116588.

XX PA

(WEIN/) WEINMURZEL H.

XX PA

(YEDA) YEDA RES & DEV CO LTD.

XX PI

Baldin M, Goltsev YV, Goncharov T, Wallach D;

XX DR

WPI; 1997-132570/12.

XX DR

P-PSDB; AAW11894.

XX PT

New DNA encoding MACH protein that interacts with MORT-1 protein - to mediate intracellular effects of FAS or TNF receptors, partic. for regulating apoptosis in tumours, virus-infected cells etc.

XX PS

Disclosure: Page 102-103; 163pp: English.

XX CC

This sequence represents the coding sequence for the mediator of cellular toxicity (MORT-1) protein. The protein encoded by this sequence is bound by the protein of the invention (see AAW11892), designated MACH. MORT-1 binds to the FAS ligand receptor (FAS-R) death domain region, and triggers part of the cell death signalling cascade in mammalian cells. Vectors containing MACH, the MACH protein, and antibodies (Ab) against it are used to modulate the effect of FAS-R ligand or TNF on cells that carry FAS-R or p55-R. This is specifically for treating tumours, HIV-infected cells or other diseased cells, by control of apoptosis/programmed cell death. The MACH protein is a mediator of the cell death pathway initiated by TNF and FAS-R binding, i.e. it mimics or enhances the effect of MORT-1 where increased cytotoxicity is required. To inhibit the effect of MORT-1, e.g. in cases of septic shock, graft rejection and acute hepatitis, sequences encoding antisense molecules or ribozymes, or Ab against MACH, are used. Compounds that inhibit MACH are potentially useful for controlling MACH activity e.g. in cases of autoimmune disease, oligodendrocyte death in multiple sclerosis or AIDS-inhibited T-cell suicide. The MACH protein can also be used to isolate and characterise other proteins and receptors involved in signalling and for Ab production. The Ab can be used to purify the new proteins and for diagnosis of conditions involving abnormal function of FAS-R mediated cellular effects.

XX CC

Sequence 1701 BP; 382 A; 459 C; 517 G; 343 T; 0 other;

		Query Match	100.0%;	Score 1701;	DB 18;	Length 1701;
		Best Local Similarity	100.0%;	Pred. No. 0;		
		Matches 1701;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	CGAGACCTGGCCAGGCGCAGGACCGGAGGACAGAGGCGCGGAGGCGCGGCGCGCAG	120			
Db	61	cgagacctggccagggccagcagcagcagcagcagcagcagcagcagcagcagcagcag	120			
Qy	121	CCCGGCGCGTTCAGACACCCGCCATGACCCGTCCTGCTGCTGCTGCTGCTGCTGCTG	180			
Db	121	ccccggccgcttgagaccgcccgccatggagccgcttccctgggtgctgctgactcgtg	180			
Qy	181	TCCAGCCTGTCGAGCAGGAGCTGACCGAGCTCAAGTTCTTATGCTCGGCGGTGGTGC	240			
Db	181	tccagcctgtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	240			
Qy	241	AAGCGCAAGCTGGAGCGGCTGCAGAGCGGCTAGACCTCTTCTCATGCTGCTGAGCAG	300			
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Qy	301	AACGACCTGGAGCCCGGCGCACACCGAGCTCCTGCGGAGCTGCTGCTGCTGCTGCTG	360			
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Qy	361	CACGACCTGCTGCGGCGGCTGCAGACCTTCGAGGCGGCGGCGGCGGCGGCGGCGCT	420			
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Qy	481	AGAAGCTGGCTGCTCAGCTCAAAGTCTCAGACACCAAGATCGACAGATCGAGGACAGA	540			
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Qy	661	GTGGCTGACCTGGTACAGAGGTTTCAGAGCGCCGCTGACCTCCAGAACAGAGTGGGGCC	720			
Db	661	gtggctgacctggtaacaagagttcagcagcccgatgacctccagaaacagagtgagtg	720			
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Qy	841	GTAGCCGACACTGTGAAGACCCAGCAGGAAGCCAGGCTGAGTGAGCCACAGACCACTG	900			
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Db	901	cttctgaactcaagctgcgtttatttaagtccctcccgccacagcagcagcagcagcagcag	960			
Qy	961	GCACAGATATTTCCATTTCTTCTCTACTATGACATGACAGAGATCTTCTCTCCACTAAA	1020			
Db	961	gcacagatatattccatttcttctcactatgacagagatcttcttctcactataa	1020			

CC which screens for proteins interacting with the Fas cytoplasmic
 CC domain. A GAL4 DNA-binding domain has been fused to the human Fas
 CC antigen cytoplasmic tail to form a bait plasmid, which is used with
 CC a prey plasmid, containing a human B-lymphocyte cDNA library fused to
 CC the GAL4 activation domain, to co-transform yeast cells.
 CC Overlapping clones 8 and 15 have been isolated, and the full-length
 CC cDNA has been isolated from a human umbilical vein endothelial cell
 CC (HUEC) library using clone 15 as a probe. The cDNA has an
 CC in-frame stop codon 130 bp upstream of the initiator Met. The
 CC encoded protein contains a death domain, with interactions with the
 CC death domain of Fas. The DNA may be used in gene therapy, and the
 CC protein or a corresponding antibody may be used to screen for
 CC agents modulating FADD pathway cellular functions and Fas-associated
 CC apoptosis, for use in therapy of e.g. AIDS, inflammation,
 CC leukemia, myocardial infarction, degenerative disease, etc.
 XX
 SQ Sequence 1642 BP; 354 A; 448 C; 508 G; 332 T; 0 other;

Query Match 95.3%; Score 1621.8; DB 17; Length 1642;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1634; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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 DB 7 aggtctcgggggtggaatcttggccgctggcaagcggcgagacctggccaggccagc 66
 QY 82 GAGCCGAGGACAGAGGCGCGGAGGCGCGGCGCGACGCCCGCGCTTCGACACCCC 141
 DB 67 gaggcggagacagaggcgacagggcgggcgagcggcgccgcttcgacacccc 126
 QY 142 GCCATGAGCCGCTTCCTGGTGTGCTGTCGACTCGGTGCTGTCAGGCTGTCGAGCAGCGAG 201
 DB 127 gccatgagccgcttcctgggtgtgctgctgcactcgggtgtcgtccagcctgtcagagcagag 186
 QY 202 CTGACCGAGCTCAAGTCTCTATGCTCGGCGCGCGTGGTCAACGGCAAGCTGAGCGCGTG 261
 DB 187 ctgaccgagctcaagtctcctaTgcctcgggcgctgggcaagcgcaagctggagcgctg 246
 QY 262 CAGAGCGGCTTAGACCTCTTCTCCATGCTGTGGAGCAGAACGACCTGGAGCCCGGGCAGC 321
 DB 247 cagagcggcctagacctctctccatgctgctgagagacgaacacctggagcccgggcac 306
 QY 322 ACCGAGCTCCTCGGCGAGCTGCTCGCCCTCCCTGCGGCGCGCAGCAGCTGCTGCGGCGCGTC 381
 DB 307 acgagctcctcgcgagctgctcctccctcctcctgcgcgccagcagcctgctggcgcgctc 366
 QY 382 GACGACTTCGAGCGGGCGGCGCGCGCGCGCGCTGGGAGAAAGCTGGCTCGTCAGCTC 441
 DB 367 gacgacttcgagcgggcgggcgggcgggcgggcgggcgggcgggcgggcgggcgggcgggcg 426
 QY 442 GCATTAAAGCTCATGTGTAATGTGGGAAAGATTGGAGAAAGCTGGCTCGTCAGCTC 501
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 DB 487 aaagtcctcagacacacaaatcgcagcatcgcagagacagatatacccccgcgaacctgacagag 546
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 QY 682 GTTCAGAGGCGCGTGAACCTCCAGACAGAGTGGGGCCATGTCCCGATGTCTATGGAAC 741
 DB 667 gttcagcagggccgtgacctccagacagagtgggggccatgtccccgagtccccgagag 726
 QY 742 TCACAGGATCTACTCCGAGCGTCTGTATGGGCGCGCTGCTTGGCGCTGGTGACACACA 801
 DB 742 TCACAGGATCTACTCCGAGCGTCTGTATGGGCGCGCTGCTTGGCGCTGGTGACACACA

DB 727 tcagagcgcatctacacctccgaagcgtcctgatggcgcgctgttgcgctgggtggaccaca 786
 QY 802 GCATCTACACAGCCTGGACTTGTCTCTCCAGGAAGGTAGCCAGACACTGTGAAGAC 861
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 DB 847 ccagcaggaagccaggctgagtgagccacagaccctgtctctgaactcaagctgctt 906
 QY 922 TATTATGCTCTCCGCGACACAGGCGGCGCTTGGGCCCTGACACAGATATTTCCATTTCTT 981
 DB 907 tattaatgctctcccgaccagggcgggcttgggccccgtgcacagatatcttccattctt 966
 QY 982 COTCACTATGACACTGAGCAAGATCTTGTCTCCACTAAATGAGCTCTCCGGGAGTACTT 1041
 DB 967 cctcaactatgacactgagcaagatctgtctccactaaatgagctcctcggggagtagctt 1026
 QY 1042 GGAAGTTGGAAACCGTGTCCAGCACAGAGGAATGTGTCAGATGAGCAGTACACTGTT 1101
 DB 1027 ggaagttggaaacctgttccagcacagaggaatctgtgcagatgagcagtcacactgtt 1086
 QY 1102 ACTCCACAGCGGAGGAGACACAGCTCAGAGGCCAGGAATCGGAGCGAGAGAGAGGTGG 1161
 DB 1087 actccacagcggagagaccagctcagaggcccggaacctggagcagagagaggtgg 1146
 QY 1162 AGAAGTGGGATTGAAACCCCGCCATCCTTCCAGCAGACCCCATGCTCAACCACTGTGGCG 1221
 DB 1147 agaactgggatttgaacccccccatccttccacagagccatgctcaacacactgtggcg 1206
 QY 1222 TTCTGCTGCCCTCCAGTTGGCAGAAAGGATGTTTTGTCCTCCATTTCTTGGAGGCGCAC 1281
 DB 1207 tctcgcgcctcctcagttggcgaaaaggatg-ttttgcctcatttctctggaggccacc 1265
 QY 1282 GGGACAGACCTGAGACTAGGCTCAGCGGGGTGCTGTGGTGGGAGAGCATGCGTGGG 1341
 DB 1266 gggacagacctggacactagggtcaggcggggtgtgtgtgggggagaggaagcggcg 1325
 QY 1342 GTGGGGTGGGAGACCTGTTGGCCGTGTCAGCTCTTGGCCCCCTGTGTGAGTTGAGT 1401
 DB 1326 gtgggggtggggagacctgtgtggcgtgtgtccagctcttggccctgtgtgagttgagt 1385
 QY 1402 CTCCTCTCTCAGACTGCTAAGTAGGGCAGTGATGGTTCGAGGACGAATTGAGATAATA 1461
 DB 1386 ctctctctcagactgctaagttaggggagcgtgtgtccagggagaaattgagataata 1445
 QY 1462 TCTGTGAGGTGCTGATGAGTGATGACACACAGCAGCTCTCTAAATCTTCTTGTGAGGAT 1521
 DB 1446 tctgtgaggtgctgagtgagtgattgacacagcagcactctctaaatcttctctgtgaggat 1505
 QY 1522 TATGGGTCTCGCAATCTACAGTTTCTTACTGTTTGTATCAAAATCAGCTATCTTCTTGA 1581
 DB 1506 taTggggtccctcgcattctcagtttcttactgttttgcatacaaaatcacatctcttctga 1565
 QY 1582 TAACAGAATTGCCAAGCGAGCGGATCTCTATCTTTAAAGAGCAGTCTCTTTATTCCTA 1641
 DB 1566 taacagaattgccaagcagcagcgggactctgtactcttcttcttcttcttcttcttctga 1625
 QY 1642 AGCTAATCTCTATTAATA 1658
 DB 1626 aggtaatcctattataaa 1642

RESULT 5
 AAX08910
 ID AAX08910 standard; cDNA; 1582 BP.
 AC AAX08910;
 XX
 DT 27-APR-1999 (first entry)
 XX Human FADD protein coding sequence.
 DE
 XX


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Oy 563 GTGTCGGGAGTCACTGAGAACTTCGGAACACACAGAGAGGAGAACGCAACAGTGGGCC 622
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 gggtaaggagagtgctgaagctgaaagatgctgagaagaagacgctcggtggccg 490
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 623 ACCTGGTGGGGCTCTCAGGTCCTCCAGATCAACCTGGTGGCTGACCTGGTACAGAGG 682
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 gactggtcaaggcgtcggaagctcagagctgaatctggtgctgacctggtggaag--- 547
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 683 TTCAGCAGCGCGTCCACCTCCAGAACAGAGGAGTGGGCCATGTCCTGGATGTCATGGAAC 742
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 -----agccaggaatctgtgacagagtgagaatatgccccagtaactaaggatt 601
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 743 CAGAGCGCATCTACCTCCGAAGCGTCTGATGGCC 777
  || || || || || || || || || || || || || || || || || || || || ||
Db 602 caactgtgtcttcctcagaaacacacctgacaagcc 636
  || || || || || || || || || || || || || || || || || || || || ||

RESULT 10
AAF90364
ID AAF90364 standard; mRNA; 298 BP.
AC AAF90364;
XX
DT 06-AUG-2001 (first entry)
DE Human FADD mRNA.
XX
KW FADD; Fas-associated death domain; human; ribozyme; gene therapy;
KW apoptosis; antiapoptotic; ss.
XX
OS Homo sapiens.
XX
FH Key
FT misc_feature 158..159 Location/Qualifiers
  /tag= a
  /note= "cleavage site of ribozyme FADD-Rz1"
FT misc_feature 167..168
  /tag= b
  /note= "cleavage site of ribozyme FADD-Rz2"
FT misc_feature 176..177
  /tag= c
  /note= "cleavage site of ribozyme FADD-Rz3"
FT misc_feature 264..265
  /tag= d
  /note= "cleavage site of ribozyme FADD-Rz4"
XX
PN EP1097993-A2.
XX
PD 09-MAY-2001.
XX
PF 03-NOV-2000; 2000EP-0250368.
XX
PR 05-NOV-1999; 99JP-0316133.
XX
PA (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
PA (TAIR/) TAIRA K.
PI Taiza K, Warashina M, Kuwabara T, Kawasaki H;
XX
DR WPI; 2001-357832/38.
XX
PT Novel chimeric molecule useful for clarifying biological function of
PT target nucleic acid and for treating viral diseases, and Alzheimer's
PT disease, comprises region with binding affinity for molecule capable of
PT sliding -
XX
PS Example 3; Fig 13C; 76pp; English.
XX
CC The present sequence is that of the 5' region of mRNA of human
CC pro-apoptotic factor FADD (Fas-associated death domain). The
CC invention provides 4 polyA-linked and -nonlinked ribozymes (see
CC AAF90365, AAF90367, AAF90369, AAF90371) aimed at specific sites
CC in this mRNA. Ribozymes FADD-Rz1, -Rz2 and -Rz3 were designed to
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CC target inaccessible sites located in a stable stem structure,
CC while ribozyme FADD-Rz4 was designed, as a control, to target a
CC relatively accessible site located in a loop region of the FADD
CC mRNA. The ribozymes were cloned into parental TRNAval-expression
CC vector pUCdT. Addition of the polyA sequence to the ribozymes
CC allowed recruitment of eIF4A1 RNA helicase, which coupled the
CC unwinding activity of the helicase to the cleavage activity of
CC the ribozymes. This facilitated cleavage of RNA previously
CC refractory to cleavage because of its high-order structure.
CC Chimeric molecules of the invention, including polyA-linked
CC ribozymes, or expression vectors, are used to prevent or treat
CC viral diseases, diseases associated with apoptosis or diseases
CC associated with abnormal gene expression (claimed). They are also
CC used in a claimed method of specifically cleaving a target nucleic
CC acid, especially a viral gene, protooncogene or a gene associated
CC with apoptosis.
XX
SQ Sequence 298 BP; 49 A; 96 C; 109 G; 44 U; 0 other;
```

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Query Match 17.0%; Score 288.8; DB 22; Length 298;
Best Local Similarity 84.9%; Pred. No. 5.6e-56;
Matches 248; Conservative 42; Mismatches 2; Indels 0; Gaps 0;
Oy 22 AGGTTCTGGGGTGAATCTTGGCGCTGGCGCAAGCGCGAGACTTGGCCAGGCCAGC 81
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 agguucgggggugaaucucugggcgugggcaagcgcgagaccugggccagggccagc 66
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 82 GAGCCGAGGACAGAGGGCGCGGAGGGCGGCGCCGCGCCGCGCCGCTTCGACAGCC 141
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 gagcgaggagagggcgacgagggcgggcgccggcgccggcgccggcgccggcgcc 126
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 142 GCATGGACCCGTTCTGTGTGCTGCTGCACTCGGTGCTGCTCAGGCTGTTCGAGCGAG 201
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 gcauaggaccuccuucugugugucugcaucugugucuccagcugucagcagcgag 186
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 202 CTGACCGAGCTCAAGTCTCTATGCTTGGCGCGGTGCTCAAGCGCAAGCTGGAGCGCTG 261
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 cugaccgagcucauguucuaugcucggcgugggcgugggcgcaagcgugagcgug 246
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 262 CAGAGCGGCTAGACCTCTTCTCCATGCTGCTGGAGCAGACAGACCTGGAGC 313
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 cagagcgccuagaccuuccauggcugugggagagcagagaccuuggagc 298
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 11
AAS54123/c
ID AAS54123 standard; DNA; 1611 BP.
XX
AC AAS54123;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #254.
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-20727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
```


Db	4045	t t c a t g t g t c t g t c t g g c g c g g g c t c a c c c a c c t c g a t g c g t g g t g g c g a c g c g	4104
QY	229	G G C G C G T G T C A A G C G C A A G C T G G A G C G C G T G C A G A G C G G C C T A G A C C T C T T C T C C A T G	288
Db	4105	a c g c g c g t c t c a a g g g a c a g g t g t c g t c g t c c t c g t c c t c o a g t t c c t g g c g c g g c g	4164
QY	289	C T G C T G G A G C A A C A C A C T G G A G C G C G G G C A C A C C G A G C T C C T G C G C G A G C T G C T C G C C	348
Db	4165	c t a c a c g c g g g t c g g c t c g a c c c g c t g c t c g c g c g t t c g c g t c g g c t g t a c t c	4234
QY	349	T C C C T G C G G C C C A C A C A C T G C T G C G G C G C G T G C A G A C T C G A G C A C T C G A G C G G G G C G C G C C	408
Db	4225	a a c a g c g t c t c t c g a c c a a c c c c t c t c t c g a c g c g t g c a g a e g c t g t g c g g g c	4284
QY	409	G G G C C G C G C C T G G G	423
Db	4285	c t c t t c g c c c t g t g	4299
 RESULT 13 AAA10594			
ID	AAA10594	standard; DNA; 10732 BP.	
AC	AAA10594;		
XX			
DT	29-JUN-2000	(first entry)	
XX			
DE	Gene encoding a subunit of cellulose synthase.		
XX			
KW	Cellulose synthase; cellulose production; increase yield; ds.		
XX			
OS	Vigna angularis.		
XX			
PN	JP2000060568-A.		
PD	29-FEB-2000.		
PF	26-AUG-1998;	987P-0239998.	
XX			
PR	26-AUG-1998;	987P-0239998.	
XX			
(MIZU/)	MIZUNO K.		
PA	(OJIP) OJI PAPER CO.		
XX			
WIPI:	2000-342371/30.		
DR	P-PSDB; AY85179.		
PT	A gene encoding a cellulose synthetic equipment - for the improvement		
XX	In the amount of cellulose synthesised in a plant body		
PS	Claim 2; Page 14-21; 32pp; Japanese.		
CC	This sequence represents a gene encoding a subunit of the cellulose		
CC	synthase complex of Vigna angularis. The invention relates to subunits		
CC	cellulose synthetic equipment, that can be used to increase the amount		
CC	cellulose synthesised by a plant. The proteins and genes encoding them		
CC	can also be used to improve the properties of the cellulose being		
CC	produced by a plant.		
XX			
SQ	Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;		
 Query Match 3.1%; Score 52.2; DB 21; Length 10732;			
Best Local Similarity 13.2%; Pred. No. 0.065;			
Matches 126; Conservative 373; Mismatches 446; Indels 12; Gaps			
QY	373	C G G C G G T C G A C A T T C G A G C G G G G C G C G G C G C C T G G G A A G A G A C	432
Db	9491	g s r n g n e s h y s g y h s r v a g h s h s r a s n v a a s r h s g h r h a e s r a s a a g y a r a s	9550
QY	433	C T G T G T G C A G C A T T T A A C G T C A T A T G T A A T C T G G G A A G A T T T G G A A G G C T G C T	492

complement related protein; cytochrome; kineasin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections

Claim 1; Page 2843; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 51 BP; 14 A; 11 C; 19 G; 7 T; 0 other;

Query Match 3.0%; Score 51; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 TCCGCGACACGCGCGGCTTGGCCCTGCACAGATATTTCCATTCTTCCT 984
|||||
Db 51 TCCGCGACACGCGCGGCTTGGCCCTGCACAGATATTTCCATTCTTCCT 1

RESULT 15
AAC75683
ID AAC75683 standard; cDNA; 1251 BP.
XX
AC AAC75683;
XX
DT 08-FEB-2001 (first entry)
DE Human ORFX ORF1238 polynucleotide sequence SEQ ID NO:2475.
XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic; vulnerable; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

9551 asyathrsrscysaagstraaasraasgashshargysygsrscysysrrvagy 9610
QY 493 CGTCAGCTCAAGACTCAGACACCAAGACTCGACAGATCGAGACAGATACCCCGCGCAAC 552
Db 9611 aasrasasnmataashvagmtgysaavavasarvagysaathrgnsrrsraasysaavat 9670
QY 553 CTGACAGAGCGGTGCGGGAGTCACTGAGAACTGGAAGAACACAGAGAGAGGAGAGCA 612
Db 9671 hrgaasnsrgrthrgythrsgsrthrggyysgrvarashsgrnthrthrgthrthr 9730
QY 613 ACAGTGGCCACCTGGTGGGGCTCTCAGTCTCGCTGCGCAGATGAACCTGGTGGCTGACCTG 672
Db 9731 rgvavaasmtgrmtasrshasrasyssysaenhrchryssrshsghythrvargytr 9790
QY 673 GTACAAGAGTTACAGAGCGCGTGCAGCTCCAGAACAGAGAGTGGGCCATGTCCCGCATG 732
Db 9791 gnavavaysthrngnashhvatrhshysgyrasashsasysvaaaahrgshvaasnaash 9850
QY 733 TCATGGAACCTCAGACGATCTACCTCCGAGCGTCTGTGATGGCGCGCTGCTTCGCGTGG 792
Db 9851 ashashsrarrgysrvahsa-----sthrngnasrrgncysrshscysrcy 9899
QY 793 TGGACACAGGCATCTACAGCGCTGACITTTGTTCTCTCCAGGAAGGTAGCCACGAC 852
Db 9900 srrasrsrvavaasnraraagygashnaasasrasyaragrgsrngasrasyssryysgva 9959
QY 853 TGTGAAGACCCAGGAGGCGGCTGAGTGAGCCACACACACCTGCTTCTCAACTCA 912
Db 9960 gargaavaasatyrasarsraasrnygyyargashartyasasngymtrthrgtyr 10019
QY 913 AGCTGCGTTTAAATGCTCTCCGACAGCGCGGCTTGGCCCTGCACAGATATTT 972
Db 10020 mtvaargvahgntyrsthrsrsgysrsvagghshvacystyrasrsgyysthrastyr 10079
QY 973 CCATTTCTCTCACTATGACACTGAGCAAGATCTGTCTCCACTAAATGAGCTCCTCGC 1032
Db 10080 snhaegyChrthraaastmtashhscysrshsrgnasvrasrmtargasaasysgshas 10139
QY 1033 GGAGTAGTGGAAAGTTGGAACCGTGTCCAGCACAGAAGGAATCTGTGCAGATGAGCAGT 1092
Db 10140 trasgthrargasrsgyysasngthrhvavagysgarghsrargasnsrstrgnvathr 10199
QY 1093 CACACTGTACTC-CACAGCGGAGGAGACACAGCTCAGAGGCCAGGATCGAGCGGAAGC 1151
Db 10200 hrrscysghasngasngygytyrtyrasngysghthrasysasysrsgsrnyysgva 10259
QY 1152 AGAGAGGTGGAGACTGGGATTGTAACCCCGCCATCTTCCACAGAGCCCATGCTCAAC 1211
Db 10260 garysgnsraathrasarggrrmtasngngsrgysthrasrarggnsrhyysgrra 10319
QY 1212 CACTGTGCGTTCCTGCTCCCTGAGTGGCAGAAAGATGTTTTGTCCCATTTCTCTT 1271
Db 10320 sngyngasngysaasngysaasnsrsgnshthrgaagysaaahsasansysvahr 10379
QY 1272 GGAGGCCACCGGACAGACCTGACACTAGGTGAGCGGGGTGCTGCTGGGGGAG 1328
Db 10380 gggaasnasraancysgggaayscysggngngsrmtsrsgysrshsasas 10436

RESULT 14
AAL31857/c
ID AAL31857 standard; DNA; 51 BP.
XX
AC AAL31857;
XX
DT 24-JAN-2002 (first entry)
DE Human SNP oligonucleotide #5065.
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

